

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 06:49:14 ; Search time 4394 Seconds  
(without alignments)  
10187.345 Million cell updates/sec

Title: US-10-661-966-1\_146001-146700\_A146311

Perfect score: 700

Sequence: 1 ctgtttcacataaagtgtttt.....gccttttagtgatggtgca 700

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 70 summaries

Database :

GenEmbl:\*

1: gb env:\*

2: gb pat:\*

3: gb ph:\*

4: gb pl:\*

5: gb pr:\*

6: gb ro:\*

7: gb sts:\*

8: gb sv:\*

9: gb un:\*

10: gb vi:\*

11: gb ov:\*

12: gb htg:\*

13: gb in:\*

14: gb om:\*

15: gb ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	698.4	99.8	127447	5	AC006344	AC006344 Homo sapi
C 2	168	24.0	197215	12	AC167793	AC167793 Bos tauru
C 3	115.6	16.5	159859	12	AC074010	AC074010 Homo sapi
4	115.6	16.5	172573	5	AC007276	AC007276 Homo sapi
5	115.2	16.5	147859	12	AC011079	AC011079 Homo sapi
6	115.2	16.5	169821	12	AC025490	AC025490 Homo sapi
7	115.2	16.5	186370	5	AC093671	AC093671 Homo sapi
8	115.2	16.5	212421	12	AC109591	AC109591 Homo sapi
9	114.4	16.3	161343	12	AC144869	AC144869 Pan trogl
10	114	16.3	135692	5	AC021134	AC021134 Homo sapi
11	114	16.3	156393	12	AC116177	AC116177 Homo sapi
12	113.2	16.2	154369	5	AC004803	AC004803 Homo sapi
13	113.2	16.2	157492	5	AC008836	AC008836 Homo sapi
14	112.8	16.1	66795	12	AC110584	AC110584 Homo sapi
15	112.8	16.1	191004	5	AC124649	AC124649 Homo sapi
16	112.8	16.1	207181	12	AC016756	AC016756 Homo sapi
17	112.8	16.1	210629	5	AC090150	AC090150 Homo sapi
C 18	112	16.0	157003	12	AC008022	AC008022 Homo sapi

19	112	16.0	166787	5	AC055723	AC055723 Homo sapi
C 20	112	16.0	183720	12	AC092912	AC092912 Homo sapi
21	112	16.0	186144	12	AC069048	AC069048 Homo sapi
C 22	111.6	15.9	601	7	BV184889	BV184889 sqm14628
C 23	110.8	15.8	758	7	BV612024	BV612024 S217P6184
C 24	110.8	15.8	182301	5	AC012498	AC012498 Homo sapi
C 25	110.6	15.8	33223	5	AC009296	AC009296 Homo sapi
C 26	110.6	15.8	168624	5	AC092131	AC092131 Homo sapi
C 27	110.6	15.8	173189	5	AC092323	AC092323 Homo sapi
28	110.4	15.8	67307	12	AC120598_3	Continuation (4 of
29	110.4	15.8	110000	12	AC120598_2	Continuation (3 of
30	110.4	15.8	141677	5	AC114492	AC114492 Homo sapi
C 31	110.4	15.8	180247	12	AC053509	AC053509 Homo sapi
32	110.2	15.7	161297	5	AC146076	AC146076 Pan trogl
C 33	110.2	15.7	173479	5	AC097520	AC097520 Homo sapi
34	110.2	15.7	187017	12	AC112190	AC112190 Homo sapi
35	110.2	15.7	203278	5	AC010482	AC010482 Homo sapi
36	110.2	15.7	242730	12	AC099408	AC099408 Pan trogl
C 37	109.8	15.7	736	7	BV639424	BV639424 S217P6156
38	109.8	15.7	30936	5	AL672206	AL672206 Human DNA
C 39	109.6	15.7	58326	12	AC108383	AC108383 Pan trogl
C 40	109.6	15.7	85836	12	AC108384	AC108384 Pan trogl
C 41	109.4	15.6	45090	5	AL450486	AL450486 Human DNA
C 42	109.4	15.6	133458	12	AL137842	AL137842 Homo sapi
43	109.4	15.6	166793	12	AC090401	AC090401 Homo sapi
C 44	109.4	15.6	167934	5	AP001034	AP001034 Homo sapi
45	109.4	15.6	178544	5	AC007538	AC007538 Homo sapi
46	109.2	15.6	31105	5	AL158174	AL158174 Human DNA
C 47	109	15.6	144147	5	AC145394	AC145394 Pan trogl
C 48	109	15.6	146098	5	AC074112	AC074112 Homo sapi
49	109	15.6	181557	12	AC072055	AC072055 Homo sapi
50	109	15.6	186616	12	AC026294	AC026294 Homo sapi
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52	108.6	15.5	107427	5	HS481A17	Z82212 Human DNA s
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57	107.8	15.4	177219	12	AC021286	AC021286 Homo sapi
C 58	107.6	15.4	117409	5	AC008400	AC008400 Homo sapi
C 59	107.6	15.4	171808	12	AC141585	AC141585 Homo sapi
C 60	107.6	15.4	172875	5	AC084301	AC084301 Homo sapi
61	107.6	15.4	189812	5	AC009410	AC009410 Homo sapi
62	107.6	15.4	203171	5	AC108116	AC108116 Homo sapi
63	107.6	15.4	206589	5	AC009483	AC009483 Homo sapi
C 64	107.6	15.4	209434	5	AC026227	AC026227 Homo sapi
65	107.6	15.4	326786	12	AC022365	AC022365 Homo sapi
66	107.4	15.3	171832	5	AC079942	AC079942 Homo sapi
67	107.2	15.3	110000	12	AC079625_0	AC079625 Homo sapi
68	107.2	15.3	110000	12	AC018743_2	Continuation (3 of
69	107	15.3	58645	5	AC002068	AC002068 Homo sapi
C 70	107	15.3	139556	5	AC079943	AC079943 Homo sapi

#### ALIGNMENTS

RESULT 1	AC006344	127447 bp	DNA	linear	PRI 21-DEC-1999
AC006344/c	Homo sapiens PAC clone	RP4-726N20	from 7q32-q34,	complete sequence.	
LOCUS	AC006344				
DEFINITION	AC006344.2	GI:4508150			
ACCESSION	AC006344				
VERSION	AC006344.2				
KEYWORDS	HTG.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo				
REFERENCE	1 (bases 1 to 127447)				
AUTHORS	Sulston, J.E. and Waterston, R.				
TITLE	Toward a complete human genome sequence				
JOURNAL	Genome Res. 8 (11), 1097-1108 (1998)				

9847074  
 2 (bases 1 to 127447)  
 Cordes, M., Wohldman, P., Pape, K. and Hovic, M.  
 The sequence of Homo sapiens PAC clone RP4-726N20  
 Unpublished  
 3 (bases 1 to 127447)  
 Waterston, R.H.  
 Direct Submission  
 Submitted (11-JAN-1999) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 4 (bases 1 to 127447)  
 Waterston, R.H.  
 Direct Submission  
 Submitted (24-MAR-1999) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 5 (bases 1 to 127447)  
 Waterston, R.  
 Direct Submission  
 Submitted (10-JUL-1999) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 6 (bases 1 to 127447)  
 Waterston, R.  
 Direct Submission  
 Submitted (21-DEC-1999) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 On Mar 24, 1999 this sequence version replaced gi:4139379.  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu/gsc>  
 Contact: [sapiens@watson.wustl.edu](mailto:sapiens@watson.wustl.edu)  
 ----- Summary Statistics  
 Center project name: H\_DJ0726N20  
 -----

NOTICE: This sequence may not represent the entire insert of this  
 clone. It may be shorter because we only sequence overlapping  
 clone sections once, or longer because we provide a small overlap  
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate  
 chemistry, or covered by high quality data (i.e., phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by sequence  
 from more than one subclone; and the assembly was confirmed by  
 restriction digest.

MAPPING INFORMATION:  
 The sequence of this clone was established as part of a mapping and  
 sequencing collaboration between the NHGRI Chromosome 7 Mapping  
 Project (Eric D. Green, Director), John D. McPherson in the  
 Department of Genetics (Washington University), and the Washington  
 University Genome Sequencing Center. For additional information  
 about the map position of this sequence, see  
<http://www.nhgri.nih.gov/DIR/OTB/CHR7>, send  
 mailto:egreen@nhgri.nih.gov, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:  
 This clone was derived from human PAC library RPCI-4, prepared by  
 Pieter de Jong and coworkers at the Roswell Park Cancer Institute  
 (<http://bacpac.med.buffalo.edu>) using the method described by  
 Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from  
 one male donor.  
 The clone may be obtained either from Genome Systems, Inc.  
 (<http://www.genomesystems.com>) or Research Genetics, Inc.  
 (<http://www.resgen.com>); or from Pieter de Jong.  
 VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:  
 The clone sequenced to the left is RP4-529P3. Actual start of this  
 clone is at base position 1 of RP4-726N20; actual end is at 127447

of RP4-726N20.  
 The run of A's from 48936 to 48936 may contain one less A, no read  
 was able to make an exact call.

FEATURES  
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 48..72  
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 1932..2231  
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Query Match 99.8%; Score 698.4; DB 5; Length 127447;			
Best Local Similarity 99.9%; Pred. No. 6.1e-194;			
Matches 699; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
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DB			
QY	121	TATATACATGCGCCATGCTGGTGTCTGCACCATTAACTCACATGAAGTTTTTTTAAA 180	
DB			
QY	181	TTTTAGTCACAGTTTTAGTCATTTTCTTAATGAAAGTATCATAGTAATCCATAAATT 240	
DB			
QY	241	GAATAAATGTTAACTACTCTGATAAAAAAGTTTATAGTTTCCCTACTTTTAAAGCAAAAT 300	
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QY	301	TCCATAGGCGATGTAATTTAGTTTCAACATTACTTGCAGTTTCAGTTAGTAATAAAT 360	
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QY	361	ATTAAGCCCTAGTAATAATTTATATGTCAAATAATTTGGAAATACCATGGGTACT 420	
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DB			
QY	481	TTTGAATATCTAGTACAGGAATATCATTTGTGTAGTTGAATTTTACGCTTAGAAAAACAAT 540	
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QY	94869	TGACACTTGGAGTAACAAATTGCGCTTTTAGGTGATGTGGCA 94830	
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LOCUS Bos taurus clone CH240-216G5, WORKING DRAFT SEQUENCE, 8 unordered			
DEFINITION pieces.			
ACCESSION AC167793.2 GI:95664410			
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.			
KEYWORDS Bos taurus (cattle)			
SOURCE Bos taurus			
ORGANISM			
REFERENCE			
AUTHORS			
Muzny,D., Adams,C., Agbai II,O., Allen,C., Albrooks,S., Archer,P.,			
Arredondo,H., Bandaranaike,D., Bangura,L., Beltran,B., Beltran,R.,			
Beraducci,A., Biswal,K., Blyth,P., Bonham,H., Buhay,C., Burch,P.,			
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Chacko,J., Chahrour,M., Chavez,D., Chen,A., Chen,G., Chen,R.,			
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KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE     1 (bases 1 to 159859)
AUTHORS      Waterston,R.H.
TITLE        The sequence of Homo sapiens clone
JOURNAL      Unpublished
AUTHORS      2 (bases 1 to 159859)
TITLE        Direct Submission
JOURNAL      Submitted (09-JUL-2000) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
COMMENT      On Aug 21, 2000 this sequence version replaced gi:9857594.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0707H02
----- Summary Statistics -----
Sequencing vector: M13; 90%
Chemistry: Dye-primer ET; 90% of reads
Assembly: Dye-terminator Big Dye; 10% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 154712 bases at least Q40
Consensus quality: 156380 bases at least Q30
Consensus quality: 157349 bases at least Q20
Insert size: 150000; agarose-fp
Insert size: 159259; sum-of-contigs
Quality coverage: 6.07 in Q20 bases; agarose-fp
Quality coverage: 5.40 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 5768: contig of 5768 bp in length
* 5769 5868: gap of unknown length
* 5869 16069: contig of 10201 bp in length
* 16070 16169: gap of unknown length
* 16170 32213: contig of 16044 bp in length
* 32214 32314: gap of unknown length
* 32314 50864: contig of 18551 bp in length
* 50865 50965: gap of unknown length
* 50965 74031: contig of 23067 bp in length
* 74032 74131: gap of unknown length
* 74132 106962: contig of 32831 bp in length
* 106963 107062: gap of unknown length
* 107063 159859: contig of 52797 bp in length.
*
* Location/Qualifiers
*   1..159859
*     /organism="Homo sapiens"
*     /mol_type="genomic DNA"
*     /db_xref="taxon:9606"
*     /chromosome="RPC1-11"
*     /clone="RP11-707H2"
*   1..5768
*     /note="assembly_name:Contig8"
*   5769..5868
*     /estimated_length=unknown
*   5869..16069
*     /note="assembly_name:Contig9"
*   16070..16169

misc_feature
gap
misc_feature
gap

FEATURES      source
             /estimated_length=unknown
             /note="assembly_name:Contig10"
             /estimated_length=unknown
             /note="assembly_name:Contig11"
             /estimated_length=unknown
             /note="assembly_name:Contig12"
             /estimated_length=unknown
             /note="assembly_name:Contig13"
             /estimated_length=unknown
             /note="assembly_name:Contig14"

ORIGIN
Query Match      16.5%; Score 115.6; DB 12; Length 159859;
Best Local Similarity 87.0%; Pred. No. 1.5e-23;
Matches 127; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGTGATTTTAAATAAATATCATTTCTTTTATTTATTATTATATCTT 75
Db 145351 TATTTTTTTTTCATGAACAGTAACATTTTATTTTATTTATTATTATTATCTT 145292

QY 76 TTAAGTTTTAGGGTACATGTGCAAAAGTGTGAGGTAGTTACATATATATATATGTCGA 135
Db 145291 TTAAGTTTTAGGGTACATGTGCAAAATGTGCAAGTGTAGTTACATATATGTCGA 145232

QY 136 TGTCTGGTGTCTGCACCACTTAACCTC 161
Db 145231 TGTCTGGTGTCTGCACCACTTAACCTC 145206

RESULT 4
AC007276 LOCUS AC007276 172573 bp DNA linear PRI 08-OCT-2003
DEFINITION Homo sapiens BAC clone RP11-22601 from 7, complete sequence.
ACCESSION AC007276
VERSION AC007276.3 GI:6587937
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 172573)
AUTHORS Sulston,J.E. and Wilson,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
PUBMED 9847074
REFERENCE 2 (bases 1 to 172573)
AUTHORS Joshua,C., Le,T., Maupin,R. and Yoakum,M.
TITLE The sequence of Homo sapiens BAC clone RP11-22601
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 172573)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (09-APR-1999) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
REFERENCE 4 (bases 1 to 172573)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-1999) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
REFERENCE 5 (bases 1 to 172573)
AUTHORS Waterston,R.
```







```
misc_feature      /estimated_length=100
                  46960..65038
                  /note="assembly_fragment"
gap              65039..65138
                  /estimated_length=100
misc_feature      65139..84585
                  /note="assembly_fragment"
                  clone_end:T7
                  vector_side:right
gap              84586..84685
                  /estimated_length=100
misc_feature      84686..111452
                  /note="assembly_fragment"
gap              111453..111552
                  /estimated_length=100
misc_feature      111553..1136123
                  /note="assembly_fragment"
gap              136124..136223
                  /estimated_length=100
misc_feature      136224..169821
                  /note="assembly_fragment"

ORIGIN
Query Match      16.5%; Score 115.2; DB 12; Length 169821;
Best Local Similarity 87.5%; Pred. No. 2e-23;
Matches 126; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 18 TTTTTCATGATGTTTAAATAATATCATTTCTTTTATATATATATATCTTTT 77
Db 27858 TTCTATTTTAAATTTTAAATAATTTTATTTTATTTTAAATATATATATCTTTT 27917

Qy 78 AAGTTTTCAGGTACATGTCAGGTCAGGTTAGTTACATATATATATATATGTCACATG 137
Db 27918 AAGTTTTCAGGTACATGTCAGGTCAGGTTAGTTACATATATATATATGTCACATG 27977

Qy 138 CTGGTGTCTGCACCCATTAATCTC 161
Db 27978 CTGGTATGTCACCCACTATCTC 28001

RESULT 7
AC093671/c      186370 bp DNA linear PRI 10-JAN-2002
DEFINITION      Homo sapiens BAC clone RP11-542P2 from 4, complete sequence.
ACCESSION      AC093671
VERSION      AC093671.3 GI:17861069
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homnidae; Homo.
REFERENCE      1 (bases 1 to 186370)
                Sulston,J.E. and Waterston,R.
                Toward a complete human genome sequence
                Genome Res. 8 (11), 1097-1108 (1998)
PUBMED      9847074
REFERENCE      2 (bases 1 to 186370)
                Holmes,A., Elliott,G. and Kozlowski,A.
                The sequence of Homo sapiens BAC clone RP11-542P2
                Unpublished (2002)
JOURNAL
REFERENCE      3 (bases 1 to 186370)
                Waterston,R.H.
                Direct Submission
                Submitted (07-SEP-2001) Genome Sequencing Center, Washington
                University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                MO 63108, USA
                4 (bases 1 to 186370)
                Waterston,R.H.
                Direct Submission
                Submitted (15-DEC-2001) Genome Sequencing Center, Washington
                University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                MO 63108, USA
```

```
REFERENCE      5 (bases 1 to 186370)
                Waterston,R.H.
                Direct Submission
                Submitted (03-JAN-2002) Genome Sequencing Center, Washington
                University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                MO 63108, USA
                6 (bases 1 to 186370)
                Waterston,R.
                Direct Submission
                Submitted (10-JAN-2002) Department of Genetics, Washington
                University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                On Dec 15, 2001 this sequence version replaced gi:16259163.
                ----- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
                Contact: sapiens@watson.wustl.edu
                ----- Summary Statistics
                -----
                Center project name: H_NH0542P02
                -----
```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

#### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

#### SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanesi,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

#### NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is AC048378; the clone sequenced to the right is RP11-5K16. Actual start of this clone is at base position 1 of RP11-542P2; actual end is at base position 186370 of RP11-542P2.

Data from AC048378, AC025490 and AC010954 was used to finish the clone, AC093671. Single plasmid region exists between 150675 and 150731.

#### FEATURES

##### source

Location/Qualifiers  
1. 186370  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="4"  
/map="4"  
/clone="RP11-542P2"  
/clone\_lib="RPCI-11"

##### misc\_feature

1. .24

##### repeat\_region

4. .295

##### misc\_feature

4. .22

/note="match to EST BM021296 (NID:gl6535652) ie75d01.y1"

/rpt\_family="Alu"



```
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-terminator; Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 209891 bases at least Q40
Consensus quality: 210714 bases at least Q30
Consensus quality: 211269 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 212031; sum-of-contigs
Quality coverage: 7.60 in Q20 bases; agarose-fp
Quality coverage: 6.42 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 4750: contig of 4750 bp in length
* 4751 4850: gap of unknown length
* 4851 39482: contig of 34632 bp in length
* 39483 39582: gap of unknown length
* 39583 68572: contig of 28990 bp in length
* 68573 68672: gap of unknown length
* 68673 92735: contig of 24063 bp in length
* 92736 92835: gap of unknown length
* 92836 131161: contig of 38326 bp in length
* 131162 131261: gap of unknown length
* 131262 212421: contig of 81160 bp in length.
* 212421 Location/Qualifiers
* 1..212421
* /organism="Homo sapiens"
* /mol_type="genomic DNA"
* /db_xref="taxon:9606"
* /chromosome="4"
* /clone="RP11-739K5"
* 1..4750
* /note="assembly_name:Contig13"
* 4751..4850
* /estimated_length=unknown
* 4851..39482
* /note="assembly_name:Contig14"
* 39483..39582
* /estimated_length=unknown
* 39583..68572
* /note="assembly_name:Contig15"
* 68573..68672
* /estimated_length=unknown
* 68673..92735
* /note="assembly_name:Contig16"
* 92736..92835
* /estimated_length=unknown
* 92836..131161
* /note="assembly_name:Contig17"
* 131162..131261
* /estimated_length=unknown
* 131262..212421
* /note="assembly_name:Contig18"
*
ORIGIN
Query Match 16.5%; Score 115.2; DB 12; Length 212421;
Best Local Similarity 87.5%; Pred. No. 1.9e-23;
Matches 126; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Qy 18 TTTTTCATGATGATTTTAAATAATATCATTTTCITTTTATTATATATACITTT 77
Db 93400 TTCTATTTTAAATTTTAAATAATTTATTTTATTTTAAATTTATTTATTTATTTT 93459
```

```
Qy 78 AAGTTTTCAGGTACATGTGCAAGTGTGCAGTTAGTTACATATATATACATGTGCCATG 137
Db 93460 AAGTTTTCAGGTACATGTGCAAGTGTGCAGTTAGTTACATATATATACATGTGCCATG 93519
Qy 138 CTGTGTGCTGTCACCCCACTTAATC 161
Db 93520 CTGTGTGCTGTCACCCCACTATCTC 93543
RESULT 9
AC144869
LOCUS
DEFINITION
Pan troglodytes clone CH251-287A2, WORKING DRAFT SEQUENCE, 7
linear
161343 bp
DNA
HTG 09-JUN-2003
ordered pieces.
AC144869
AC144869.2 GI:31544080
HTG; HTGS PHASE2; HTGS DRAFT.
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
REFERENCE
1 (bases 1 to 161343)
Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K.,
Chu,G., Coleman,B., Coleman,H., Engle,J., Granite,S., Guan,X.,
Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P.,
Hurle,B., Iqbal,J.R., Karlins,E., Kwong,P., Laric,P., Lee-Lin,S.-Q.,
Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masello,C.,
Maskeri,B., McDowell,J., Paguirigan,C., Pearson,R., Portnoy,M.E.,
Prasad,A., Reddi-Dugue,N., Schandler,K., Schueler,M.G., Shah,K.,
Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V.,
Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.
NSC Comparative Sequencing Initiative
UNPUBLISHED
2 (bases 1 to 161343)
Green,E.D.
Direct Submission
Submitted (23-MAY-2003) NIH Intramural Sequencing Center, 8717
Government Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 161343)
Green,E.D.
Direct Submission
Submitted (09-JUN-2003) NIH Intramural Sequencing Center, 8717
Government Circle, Gaithersburg, MD 20877, USA
On Jun 9, 2003 this sequence version replaced gi:31044282.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.zoo@nhgri.nih.gov
----- Project Information
Center project name: esc
Center clone name: 287A02
The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is based on at least 8X average
coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator; Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 160248 bases at least Q40
Consensus quality: 160506 bases at least Q30
```

Consensus quality: 160675 bases at least Q20  
Insert size: 178000; agarose-fp  
Insert size: 160743; sum-of-contigs  
Quality coverage: 10.74x in Q20 bases; agarose-fp  
Quality coverage: 11.89x in Q20 bases; sum-of-contigs

\*\*\*\*\*  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 7 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.

\* This sequence will be replaced

\* by the finished sequence as soon as it is available and

\* the accession number will be preserved.

1 25268: contig of 25268 bp in length  
25269 25368: gap of unknown length  
25369 40449: contig of 15081 bp in length  
40450 40549: gap of unknown length  
40550 47926: contig of 7377 bp in length  
47927 48026: gap of unknown length  
48027 55497: contig of 7471 bp in length  
55498 55597: gap of unknown length  
55598 92427: contig of 36830 bp in length  
92428 92527: gap of unknown length  
92528 96210: contig of 3683 bp in length  
96211 96310: gap of unknown length  
96311 161343: contig of 65033 bp in length.

## FEATURES

source	Location/Qualifiers
misc_feature	1..161343 /organism="Pan troglodytes" /mol_type="genomic DNA" /db_xref="taxon:9598" /clone="CH251-287A2" /clone_lib="CH251"
misc_feature	1..85615 /note="clone overlaps with GenBank Accession Number AC099408 clone RP43-44D23 (center project name cmb)"
gap	1..25268 /note="assembly_fragment clone end:T7 vector side:left"
misc_feature	25269..25368 /estimated_length=unknown 25369..40449 /note="assembly_fragment"
gap	40450..40549 /estimated_length=unknown
misc_feature	40550..47926 /note="assembly_fragment"
gap	47927..48026 /estimated_length=unknown
misc_feature	48027..55497 /note="assembly_fragment"
gap	55498..55597 /estimated_length=unknown
misc_feature	55598..92427 /note="assembly_fragment"
gap	92428..92527 /estimated_length=unknown
misc_feature	92528..96210 /note="assembly_fragment"
gap	96211..96310 /estimated_length=unknown
misc_feature	96311..161343 /note="assembly_fragment clone end:SP6 vector_side:right"

## ORIGIN

Query Match 16.3%; Score 114.4; DB 12; Length 161343;  
Best Local Similarity 83.3%; Pred. No. 3.4e-23;  
Matches 130; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY	6	TCACATAAAGTTTTTTTTTTTTCATCATTTTATAAAATATCATTTTCTTTTATTAT 65
Db	77227	TAAATTAACAATGGTTTTTTTTTTCATGTAACAGTAACATTTTATTTTATTATAT 77286
QY	66	TATTATACTTTTTAAGTTTTTAGGTTACATGTCACAAAGTGCAGGTTAGTTACATATAT 125
Db	77287	TATTATACTTTTTAAGTTTTTAGGTTACATGTCACAAATGTCAGGTTAGTTACATATAT 77346
QY	126	ACATGTGCCATGCTGCTGTGCTGCACCCCACTTAATC 161
Db	77347	ACATGTGCCATGCTGCTGTGCTGCACCCCACTTAATC 77382

## RESULT 10

AC021134	LOCUS	AC021134	135692 bp	DNA	linear	PRI 09-JAN-2002
AC021134	DEFINITION	Homo sapiens BAC clone RP11-402D23 from 4, complete sequence.				
AC021134	ACCESSION	AC021134				
AC021134.8	VERSION	GI:14702086				
HTG.	KEYWORDS					
Homo sapiens (human)	SOURCE					
Homo sapiens	ORGANISM					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	REFERENCE	1 (bases 1 to 135692)				
Sulston,J.E. and Waterston,R.	AUTHORS					
Toward a complete human genome sequence	TITLE					
Genome Res. 8 (11), 1097-1108 (1998)	JOURNAL					
9847074	PUBMED					
2 (bases 1 to 135692)	REFERENCE					
Haglund,K., Kozlowski,A., Hawkins,M. and Spalding,L.	AUTHORS					
The sequence of Homo sapiens BAC clone RP11-402D23	TITLE					
Unpublished (2001)	JOURNAL					
3 (bases 1 to 135692)	REFERENCE					
Waterston,R.H.	AUTHORS					
Direct Submission	TITLE					
Submitted (14-JAN-2000) Genome Sequencing Center, Washington	JOURNAL					
University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	REFERENCE					
4 (bases 1 to 135692)	REFERENCE					
Waterston,R.H.	AUTHORS					
Direct Submission	TITLE					
Submitted (12-JUL-2001) Genome Sequencing Center, Washington	JOURNAL					
University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	REFERENCE					
5 (bases 1 to 135692)	REFERENCE					
Waterston,R.	AUTHORS					
Direct Submission	TITLE					
Submitted (09-JAN-2002) Department of Genetics, Washington	JOURNAL					
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA	REFERENCE					
On Jul 12, 2001 this sequence version replaced gi:14573744.	COMMENT					
-----						
Center: Washington University Genome Sequencing Center						
Center code: WUGSC						
Web site: http://genome.wustl.edu/gsc						
Contact: sapiens@wustl.wustl.edu						
-----						
Summary Statistics						
-----						
Center project name: H_NH0402D23						
-----						

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by





```
Matches 137; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
Qy 5 TTACATATAAGTTTCTTTTGTGATGATTTTAAATAAATATCATTTTCTTTTATTATTA 64
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 114844 TTCACAGGATTAATTTCTTTTATTGTTCTTAAT-TTATTTTATTATTTTATTATTA 114902
Qy 65 TTATTATACCTTTTAAGTTTATAGGTACATGTGCAGGTTAGTTACATATATA 124
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 114903 TTATTTACCTTTAAAGTTTATAGGTACATGTGCAGGTTAGTTACATATGTA 114962
Qy 125 TACATGTGCATGCTGTGTGCTGCACCCCACTTAACCTCA 162
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 114963 TACATGTGCATGCTGTGTGCTGCACCCCACTTAACCTCA 115000

RESULT 11
AC116177 156393 bp DNA linear HTG 25-MAR-2002
LOCUS Homo sapiens chromosome UNK clone RP11-527M7, *** SEQUENCING IN
DEFINITION PROGRESS ***, 2 unordered pieces.
ACCESSION AC116177.1 GI:19703339
VERSION HTG; HTGS PHASE1.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 156393)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 156393)
Waterston,R.H.
Direct Submission
Submitted (25-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
```

## COMMENT

```
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H NH0527M07
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 156145 bases at least Q40
Consensus quality: 156237 bases at least Q30
Consensus quality: 156287 bases at least Q20
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 71770: contig of 71770 bp in length
* 71771 71870: gap of unknown length
* 71871 156393: contig of 84523 bp in length.
Location/Qualifiers
1..156393
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="UNK"
/clones="RP11-527M7"
```

## FEATURES

source

```
misc_feature 1..71770
/notes="assembly_name:Contig54
clone_end:17
vector_side:left"
gap 71771..71870
/estimated_length=unknown
misc_feature 71871..156393
/notes="assembly_name:Contig55
clone_end:SP6
vector_side:right"

ORIGIN
Query Match 16.3%; Score 114; DB 12; Length 156393;
Best Local Similarity 86.7%; Pred. No. 4.5e-23;
Matches 137; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
Qy 5 TTACATATAAGTTTCTTTTGTGATGATTTTAAATAAATATCATTTTCTTTTATTATTA 64
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 65 TTATTATACCTTTTAAGTTTATAGGTACATGTGCAGGTTAGTTACATATATA 124
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RESULT 12
AC004803 154369 bp DNA linear PRI 25-FEB-2003
LOCUS Homo sapiens 12 BAC RP11-359B12 (Roswell Park Cancer Institute
DEFINITION Human BAC Library) complete sequence.
ACCESSION AC004803
VERSION AC004803.11 GI:28557808
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 154369)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralunge,H.C., Arc,J.R., Ayele,M., Banks,T.,
Barbata,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 06:41:39 ; Search time 517 Seconds  
(without alignments)  
940.182 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
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Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 70 summaries

Database : N\_Geneseq 8.\*  
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13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*  
15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	113.2	16.2	19167	5	ABR19101	Abal9101 Human ner
5	113.2	16.2	155225	12	ADQ59197	Adq59197 MSI-H car
6	106.8	15.3	8766	12	ADJ12500	Adj12500 DNA fragm
7	106.6	15.2	8666	4	AAS46305	Aas46305 Tumour su
8	106.6	15.2	8666	6	ABL32396	Ab132396 Human imm
9	106.6	15.2	8666	6	ABK34008	Abk34008 Human DNA
10	106.6	15.2	8666	6	ABQ67177	Abq67177 Human ang
11	106.6	15.2	8666	10	ADB54111	Adb54111 Pretreate
12	106.6	15.2	8666	10	ADB54239	Adb54239 Pretreate
13	106.6	15.2	8666	10	ADE84177	Ades84177 Human lym
14	106.6	15.2	8666	10	ADE84101	Ades84101 Human lym
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16	106.6	15.2	8666	13	ADS89267	Ads89267 Oligonuc1
17	105.6	15.1	70043	12	ADO48201	Ado48201 Human p21
C 18	105.4	15.1	82938	6	ABV72623	Abv72623 Human tra

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20	104.6	14.9	72678	13	ABD33207		Abd33207 Human can
C 21	104.2	14.9	42595	12	ADJ12615		Adj12615 DNA fragm
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C 31	103.2	14.7	24132	4	AAK68729		Aak68729 Human 1mm
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ALIGNMENTS

RESULT 1  
ADY94258

ID ADY94258 standard; DNA; 190276 BP.

AC ADY94258;  
DT 16-JUN-2005 (first entry)

XX BRAF protein kinase gene DNA sequence.

DE B-Raf protein kinase; melanoma; cytostatic; diagnosis; DNA polymorphism;

XX drug screening; chromosome-7q34; gene therapy; BRAF; ds; gene;

XX single nucleotide polymorphism; SNP.

OS Homo sapiens.

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PH Key Location/Qualifiers  
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FT /standard\_name= "Single nucleotide polymorphism"  
XX WO2005027710-A2.  
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XX 31-MAR-2005.  
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XX 11-SEP-2003; 2003WO-US028788.  
XX  
XX 11-SEP-2002; 2002US-0410595P.  
XX 29-OCT-2002; 2002US-0422344P.  
XX (SEQU-) SEQUENOM INC.  
XX  
XX Roth RB, Nelson MR, Braun A;  
XX WPI; 2005-273028/28.  
XX  
XX Identifying a subject at risk of melanoma, useful for treating or  
XX preventing melanoma by detecting the presence or absence of one or more  
XX polymorphic variations associated with melanoma in a nucleic acid sample  
XX from a subject.  
XX  
XX Claim 1; SEQ ID NO 1; 175pp; English.  
XX  
XX The new invention relates to the discovery that polymorphic variations in  
XX a gene (ADY94258) encoding a BRAF protein kinase is associated with the  
XX occurrence of melanoma. BRAF is a serine/threonine protein kinase and is  
XX a member of the RAF family. It participates in the RAS/RAF/MEK/ERK/MAP  
XX kinase signal transduction pathway. The BRAF gene is located on  
XX chromosome 7q34 (assembly 30). Provided are methods of identifying a  
XX subject at risk of melanoma by detecting the presence or absence of one  
XX or more polymorphic variations in BRAF associated with melanoma in a  
XX nucleic acid sample from a subject. Also disclosed is a method of  
XX identifying a polymorphic variation associated with melanoma proximal to  
XX an incident polymorphic variation associated with melanoma. Also  
XX disclosed is a method of identifying a candidate molecule that modulates  
XX cell proliferation by introducing a test molecule to a system which

CC comprises the nucleic acid; and determining the presence or absence of an  
CC interaction between the test molecule and the nucleic acid or protein.  
CC The polymorphic variations are detected at one or more positions in  
CC ADY94258. The positions are in linkage disequilibrium with one or more  
CC positions in SEQ ID No. 1, or the variation is the haplotype CTGG or ATGA  
CC in ADY94258. Detecting the presence or absence of the one or more  
CC polymorphic variations comprises hybridizing an oligonucleotide to the  
CC nucleic acid sample, where the oligonucleotide hybridizes to a region  
CC adjacent to the polymorphic variation. The proximal polymorphic variation  
CC is within a region between about 5 kb 5' of the incident polymorphic  
CC variation and about 5 kb 3' of the incident polymorphic variation.  
CC Treating melanoma in a subject alternatively comprises contacting one or  
CC more cells of a subject with a duplex RNA nucleic acid. The invention is  
CC useful for treating or preventing melanoma. The present sequence is the  
CC DNA sequence of the human BRAF gene.  
XX

SQ Sequence 190276 BP; 55599 A; 35097 C; 37143 G; 62425 T; 0 U; 12 Other;

Query Match 100.0%; Score 700; DB 14; Length 190276;  
Best Local Similarity 99.9%; Pred. No. 5e-110; 0; Mismatches 0; Gaps 0;  
Matches 699; Conservative 1; Indels 0; Gaps 0;  
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Qy 61 ATTATTATTATCTTTTAAGTTTGTAGGTACATGTCGCAAGTGTGCAGGTAGTACATA 120  
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RESULT 2  
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ID AAL05340 standard; DNA; 19167 BP.  
XX AC AAL05340;  
XX DT 21-NOV-2001 (first entry)  
XX DE Human reproductive system related antigen DNA SEQ ID NO: 8028.  
XX KW Human; reproductive system related antigen; reproductive system disorder;  
XX KW cancer; gene therapy; ds.  
XX OS Homo sapiens.  
XX PN WO200155320-A2.  
XX PD 02-AUG-2001.  
XX PF 17-JAN-2001; 2001WO-US001339.  
XX PR 31-JAN-2000; 2000US-0179065P.  
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PR 08-NOV-2000; 2000US-0246611P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249246P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 01-DEC-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 05-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.



CC sequences can be used in the treatment of cardiovascular, urinary system,  
CC reproductive system, immune, respiratory, neurological and  
CC gastrointestinal disorders, infections, and particularly cancer,  
CC especially testicular cancers. The present sequence is a DNA encoding a  
CC protein fragment of the invention  
XX  
SQ Sequence 19167 BP; 5824 A; 3876 C; 3875 G; 5592 T; 0 U; 0 Other;  
Query Match 16.2%; Score 113.2; DB 4; Length 19167;  
Best Local Similarity 82.3%; Pred. No. 2.1e-10;  
Matches 130; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
Qy 4 TTTCACATAAAAGTTTTTTTTTTTGGATGATTTTAAATAAATATCATTTTTCTTTTTTTTAT 63  
Db 10109 TTATAACTAAGTTTTTTTTTTTGGCTTGGAACTTTTTTTTAAATTTAT 10050  
Qy 64 ATTATTATACTTTTTAAGTTTTTAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATAT 123  
Db 10049 ATTATTATACTTTTTAAGTTTTTAGGTACATGTGCAACAGTGCAGGTTGTACATATGT 9990  
Qy 124 ATACATGTGCCATGCTGGTGTGCTGCACCCATTAATTC 161  
Db 9989 ATACATGTGCCATGCTGGTGTGCTGCACCCATTAATTC 9952  
RESULT 4  
ID ABA19101 standard; DNA; 19167 BP.  
XX ABA19101;  
XX  
XX 23-JAN-2002 (first entry)  
XX Human nervous system related polynucleotide SEQ ID NO 11432.  
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
KW antiparkinsonian; antiscikling; antianaemic; antiarthritic; cancer;  
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;  
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.  
XX Homo sapiens.  
XX  
XX WO200159063-A2.  
XX 16-AUG-2001.  
XX 17-JAN-2001; 2001WO-US001334.  
XX 31-JAN-2000; 2000US-0179065P.  
XX 04-FEB-2000; 2000US-0180628P.  
XX 24-FEB-2000; 2000US-0184664P.  
XX 02-MAR-2000; 2000US-0186350P.  
XX 16-MAR-2000; 2000US-0189874P.  
XX 17-MAR-2000; 2000US-0190076P.  
XX 18-APR-2000; 2000US-0198123P.  
XX 19-MAY-2000; 2000US-0205515P.  
XX 07-JUN-2000; 2000US-0209467P.  
XX 28-JUN-2000; 2000US-0214886P.  
XX 30-JUN-2000; 2000US-0215135P.  
XX 07-JUL-2000; 2000US-0216647P.  
XX 07-JUL-2000; 2000US-0216880P.  
XX 11-JUL-2000; 2000US-0217487P.  
XX 11-JUL-2000; 2000US-0217496P.  
XX 14-JUL-2000; 2000US-0218290P.  
XX 26-JUL-2000; 2000US-0220963P.  
XX 26-JUL-2000; 2000US-0220964P.  
XX 14-AUG-2000; 2000US-0224518P.  
XX 14-AUG-2000; 2000US-0224519P.  
XX 14-AUG-2000; 2000US-0225213P.  
XX 14-AUG-2000; 2000US-0225214P.

PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241783P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 06-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251473P.  
PR 08-DEC-2000; 2000US-0251858P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-483232/52.  
XX  
XX Nucleic acids encoding 973 human testicular antigen polypeptides, useful  
XX for preventing, diagnosing and/or treating testicular cancer.  
XX  
XX Disclosure; SEQ ID NO 2861; 766pp; English.  
XX  
XX The present invention provides the protein and coding sequences of 973  
XX human testicular antigens, and fragments of their genomic sequences. The  
CC





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SQ Sequence 155225 BP; 44334 A; 29321 C; 30431 G; 51139 T; 0 U; 0 Other;
Query Match 16.2%; Score 113.2; DB 5; Length 19167;
Best Local Similarity 82.3%; Pred. No. 2.1e-10;
Matches 130; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 4 TTTCCATATAAGTGTGTTTTTTTTTTTGGATGATTTTAAATAAAATATCATTTCTTTTTTTTATT 63
Db 9059 TTATAACTAACTTTTTTTTTTTTTTTTGGCTTGGAAATCTTTTTTTTAAATTTATT 9118
QY 64 ATTATTATACCTTTTAAGTTTGGGTACATGTGCAAGTGCAGGTTAGTTACATATAT 123
Db 9119 ATTATTATACCTTTTAAGTTTGGGTACATGTGCAAGTGCAGGTTTGTACATATGT 9178
QY 124 ATACATGTGCCATGCTGGTGTGCTGCACCCCACTTAACCTC 161
Db 9179 ATACATGTGCCATGTTGGTGTGCTGCACCCCACTTAACCTC 9216

RESULT 5
ADQ59197
ID ADQ59197 standard; DNA; 155225 BP.
XX
AC ADQ59197;
XX
DT 09-SEP-2004 (first entry)
XX
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:34.
XX
KW coding mononucleotide repeat; cMNR; gene; antibody; MSI-H tumour;
KW MSI-H carcinoma; high microsatellite instability tumour;
KW high microsatellite instability carcinoma; cytostatic; ds.
XX
OS Homo sapiens.
XX
FN KR2004008012-A.
XX
PD 28-JAN-2004.
XX
PF 15-JUL-2002; 2002KR-00041304.
XX
PR 15-JUL-2002; 2002KR-00041304.
XX
PA (KIMH/) KIM H G.
PA (KIMN/) KIM N G.
PA (LEEJ/) LEE J S.
PA (RHEE/) RHEE H S.
XX
PI Kim HG, Kim NG, Lee JS, Rhee HS;
XX
WPI; 2004-386326/36.
XX
Genes containing coding mononucleotide repeats are useful in developing
PT an antibody against MSI-H (hugh (sic high) microsatellite instability)
PT tumor.
XX
Claim 3; SEQ ID NO 34; 578bp; Korean.
XX
The present invention describes genes containing coding mononucleotide
CC repeats (cMNRs). The genes are useful for the development of an antibody
CC against MSI-H (hugh microsatellite instability) tumour. Also described:
CC (1) cDNA genes containing cMNRs with 10 or more nucleotide sequences, and
CC selected from the cDNA genes having the nucleotide sequences of SEQ ID
CC NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35,
CC 37, 39, 41 and 43; (2) cDNA genes, which are frameshift mutated by
CC deletion or insertion of one or more base in the cMNRs; (3) genomic DNA
CC genes containing cMNRs with 10 or more nucleotide sequences, and selected
CC from the genomic DNA genes having the nucleotide sequences of SEQ ID
CC NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36,
CC 38, 40, 42 and 44; and (4) genomic DNA genes, which are frameshift
CC mutated by deletion or insertion of one or more base in the cMNRs. The
CC genes have cytostatic activity. The present sequence represents an MSI-H
CC carcinoma genomic DNA sequence from the present invention.
XX

SQ Sequence 155225 BP; 44334 A; 29321 C; 30431 G; 51139 T; 0 U; 0 Other;
Query Match 16.2%; Score 113.2; DB 12; Length 155225;
Best Local Similarity 82.3%; Pred. No. 2e-10;
Matches 130; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 4 TTTCCATATAAGTGTGTTTTTTTTTTTGGATGATTTTAAATAAAATATCATTTCTTTTTTTTATT 63
Db 138460 TTATAACTAACTTTTTTTTTTTTTTTTGGCTTGGAAATCTTTTTTTTAAATTTATT 138519
QY 64 ATTATTATACCTTTTAAGTTTGGGTACATGTGCAAGTGCAGGTTAGTTACATATAT 123
Db 138520 ATTATTATACCTTTTAAGTTTGGGTACATGTGCAAGTGCAGGTTTGTACATATGT 138579
QY 124 ATACATGTGCCATGCTGGTGTGCTGCACCCCACTTAACCTC 161
Db 138580 ATACATGTGCCATGTTGGTGTGCTGCACCCCACTTAACCTC 138617

RESULT 6
ADJ12500
ID ADJ12500 standard; DNA; 8766 BP.
XX
AC ADJ12500;
XX
DT 20-MAY-2004 (first entry)
XX
DE DNA fragment of a BAC clone that encodes a human secreted protein Seq354.
XX
KW human; secreted; cancer; haematopoietic disease; anaemia;
KW multiple myeloma; reproductive system disorder; prostatitis;
KW inguinal hernia; musculoskeletal disease; systemic lupus erythematosus;
KW gout; cardiovascular disease; arrhythmia; hypernatraemia; fetal disease;
KW fetal alcohol syndrome; Down's syndrome; excretory disease;
KW urinary incontinence; renal disorder; neural; sensory disease;
KW Alzheimer's disease; meningitis; respiratory disease; emphysema;
KW occupational lung disease; endocrine disease; diabetes;
KW glomerulonephritis; digestive disease; portal hypertension;
KW irritable bowel syndrome; epithelial disease; scleroderma;
KW epidermolysis bullosa; cytostatic; antianemic; antiarthritic;
KW antiasthmatic; anti-HIV; immunosuppressive; antiinflammatory;
KW antipsoriatic; antibacterial; osteopathic; dermatological; antigout;
KW immunomodulator; antiarrhythmic; cardiac; nootropic; antilipemic;
KW nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer;
KW antidiabetic; anabolic; hypertensive; vulnery; ds.
XX
OS Homo sapiens.
XX
FN US2004010132-A1.
XX
PD 15-JAN-2004.
XX
PF 30-OCT-2001; 2001US-00984429.
XX
PR 09-OCT-1997; 97US-0061463P.
PR 09-OCT-1997; 97US-0061527P.
PR 09-OCT-1997; 97US-0061529P.
PR 09-OCT-1997; 97US-0061532P.
PR 09-OCT-1997; 97US-0061536P.
PR 09-OCT-1997; 97US-0071498P.
PR 08-OCT-1998; 98WO-US021142.
PR 08-APR-1999; 99US-00288143.
PR 01-NOV-2000; 2000US-0244591P.
XX
(ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (DUAN/) DUAN R D.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (GREE/) GREENE J M.
PA (YOUN/) YOUNG P E.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
```



Qy	252	TAAC	TACTCTCGAT	AAAAAAGTTTATAGTTTCCTACTCTTTTAAGC	AAATTCCTATAGGCA	311
Db	1786	AGAG	TAAATGGTTTATTTAAAGATGTTAATATTTTTTTAGAGTTTATTTAGTAAGATAT	1845		
Qy	312	TGGT	AATTTGTAAGTTTCAACATTA	CTCGCAGTTCAGTTAGTAATAATAATTAAGCCTAG	371	
Db	1846	GAGAT	ATATATTTTAAATTTGTTTTGGTAATTTTTTAAAGTAGTGAATTTTTTATATTTG	1905		
Qy	372	TAAG	TATATAATTTAATATTTGTCAAAATAATTTGGAAAAATACCATGGGTACTTTAAATGATTTT	431		
Db	1906	TTTATA	TATGTAATTTAAATGTTGTTTTATATGTTGTATTTTTTATTTTTTTTATTAATA	1965		
Qy	432	ACCA	ATTTCCATCGAACAAACAAGTTGGCTATTTTTTCGGATGTAATTTTGAATACT	491		
Db	1966	GTTA	TATATATATTTTTTTTAAAGAGTTGAAAGAGTTTTTTGATGTAGGAATTTATGCTAGAGT	2025		
Qy	492	AGTA	ACGGAATATCATTTGTTAGTTGGAATTTTTAGCCTTAGAAAACAATCGAGTTTAGAT	551		
Db	2026	TTTAG	AGAAATTTTGAATTTATTTGAAAGTTTTATTTAGAAATATATGCTGAAGTAATA	2085		
Qy	552	AGCT	AAAGTATAATTTATTTTGTGATTTTAATAATGGTATGGAGTTTAGGCCTATGATAATTA	611		
Db	2086	TATTTTTTTT	AAAAAAATTAATTAATTTATTTTTTTTTTTCGAGAAGAGTATTTATTTTA	2145		
Qy	612	GTGA	AAACACCCGAAGATGTTTTATACCTTTTAAATTT	648		
Db	2146	ATAGA	TTTTTTTGAAGGAGTTTATTTTTTTTTTATTTTTTTT	2182		

RESULT 8	
ABL32396	
ID	ABL32396 standard; DNA; 8666 BP.
XX	
AC	ABL32396;
XX	
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Human immune system associated gene SEQ ID NO: 369.
XX	
KW	Human; immune system disease; cytosine methylation; antiasthmatic;
KW	antiarteriosclerotic; antinaemic; cytostatic; nootropic;
KW	neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW	anti rheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW	antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
ds.	
XX	
OS	Homo sapiens.
XX	
PN	WO200200928-Å2.
XX	
PD	03-JAN-2002.
XX	
PF	02-JUL-2001; 2001WO-EP007537.
XX	
PR	30-JUN-2000; 2000DE-01032529.
PR	01-SEP-2000; 2000DE-01043826.
XX	
XX	(EPIG-) EPIGENOMICS AG.
PA	
XX	
PI	Olek A, Piepenbrock C, Berlin K;
XX	
DR	WPI; 2002-130909/17.
XX	
XX	
PT	Nucleic acid comprising fragment of chemically modified gene, useful for
PT	diagnosis and treatment of diseases associated with abnormal cytosine
PT	methylation.
XX	
XX	
PS	Claim 1; SEQ ID NO 369; 32pp + Sequence Listing; German.
XX	
CC	The present invention provides a number of human immune system associated
CC	genes which are modified by the methylation of cytosines. The sequences

CC	can be used in the diagnosis and treatment of immune system disorders,	
CC	including eye diseases such as retinopathy, neovascular glaucoma and	
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid	
CC	leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,	
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel	
CC	diseases. The present sequence is a gene of the invention	
XX		
SQ	Sequence 8666 BP; 2444 A; 168 C; 1868 G; 4186 T; 0 U; 0 Other;	
	Query Match 15.2%; Score 106.6; DB 6; Length 8666;	
	Best Local Similarity 49.0%; Pred. No. 2.9e-09;	
	Matches 312; Conservative 0; Mismatches 324; Indels 1; Gaps 1;	
Qy	12 AAAGTCTTTTCTTTTTCATCAATTTTAATAAAATACATTTCTTTTATTATTATTAT 71	
Db		
1547	AAAGTTTTTTATATATTATTAATAATTTTATATAATATTTTTTAATTTTATTATTATTTA 1606	
Qy	72 ACTTTTAAGTTTTAGGGTACATGTCAAAAGTGCAGGTAGTTACATATATATACATGT 131	
Db		
1607	TATTTTAAGTTTTAGAGTATATGTTATATATGTTAGGTTTGTATATATGTTATATGT 1666	
Qy	132 GCATGCTGCTGTCGCACCAATTAACACATGAAGTTTTTTTTTAAATTTTAGTGACA 191	
Db		
1667	GTTATGTTGCTGTTGTATTTATTAATAATTATTA-TTATTTAGTATTAGGTATATTTTAAAT 1725	
Qy	192 GTTTTGTCTCAATTTTCCCTAAATGAAAGTATCATAACTCAATAATTTTGAAAAAATGT 251	
Db		
1726	GTTATTTTCTTTTCTTTTCTTTTATATAAGATTTATAATGGATTAATGGATTTTAAATTTT 1785	
Qy	252 TAACACTCTGATAAAAAAGTTTTATAGTTTCCTACTTTTAAGCAAAATTCCTATAGGCCA 311	
Db		
1786	AGAGTAAATGGTTTTATTTTAAGGATGTTATATAATTTTTTTTAGAGTTTATATGTAAGATAT 1845	
Qy	312 TGGTAATTTGAGTTTCAACATTACTTTCGAGTTTCAGTTAGTAAATAAAATTAAGCCTAG 371	
Db		
1846	GAGATATATATTTAAATAATTTGTTTGGTATTTTAAAGTAGTTAAATTTTATATTG 1905	
Qy	372 TAAGTATAATTTTAATATGTGCAAAATAATTTGGAAAATACCATGGGTACTTAATGATTTT 431	
Db		
1906	TTTATAATGTTATTAATAATGTTGTTTTATATGCTTGTATTTTTTATTTTTTTTATTAAATA 1965	
Qy	432 ACCAAATTTCCATGGCAACAAACAGGTGCTATTTTTTGGATTGATATTTTGCATAACT 491	
Db		
1966	GTTATATATATTTTTTATAAGAGTTGAAGAGTTTTTGTAGTAGGAATTTATGCTAGAGT 2025	
Qy	492 AGTACAGGAATCATTTGTTAGTTGAATTTTTTAGCCCTAGAAAACAAAATCGAGTTTAGAT 551	
Db		
2026	TTTAGAGAAATTTTGAAATTTATTTGAAAGTTTTTATTTAGAAATATATGTGTAAAGTGAATA 2085	
Qy	552 AGCTAAAGTATAATTTATTTGTCATTTAATAATGTTATGGAGTTTAGGGCTATCATTAATTA 611	
Db		
2086	TATTTTTTTTAAAAAAATTAATTAATTTATTTTTTTTTTTTTTTTGAGAAGAGGTATTTATTTTA 2145	
Qy	612 GTGAAACACCCCAAGATGTTTTATACTTTTAAATTT 648	
Db		
2146	ATAGATTTTTTGAAGGAGTTTATTTTTTTTATTTTTTT 2182	

RESULT 9	
ABK34008	
ID	ABK34008 standard; DNA; 8666 BP.
XX	
XX	
AC	ABK34008;
XX	
DT	18-JUN-2002 (first entry)
XX	
DE	Human DNA for staging of Astrocytomas #48.
XX	
XX	Human; ds; astrocytoma; cytosstatic; staging; cystein
KW	bisulphite; brain tissue; MALDI; ESI; electron spr
KW	matrix assisted laser desorption/ionization mass sp
XX	
OS	Homo sapiens.
XX	

XX PN WO200202808-A2.  
 XX PD 10-JAN-2002.  
 XX PF 02-JUL-2001; 2001WO-EP007538.  
 XX PR 30-JUN-2000; 2000DE-01032529.  
 XX PR 01-SEP-2000; 2000DE-01043826.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX DR WPI; 2002-171649/22.  
 XX PT Novel chemically modified genomic DNA sequences, useful in the  
 PT characterization, classification, differentiation, grading, staging,  
 PT treatment and/or diagnosis of astrocytomas or predisposition to  
 PT astrocytomas.  
 XX PS Claim 1; SEQ ID NO 95; 37pp; English.  
 XX CC The invention relates to a nucleic acid comprising a sequence (I) of at  
 CC least 18 bases in length of a segment of chemically pre-treated genomic  
 CC DNA which has any one of the sequences of (ABK33919-ABK34032) or its  
 CC complement. Also included are an oligonucleotide or peptide nucleic acid  
 CC (or set thereof) of at least 9 nucleotides which hybridises to (I),  
 CC primers for (II), probes for detecting cytosine methylation or single-  
 CC nucleotide polymorphisms (SNP) in (I), an array of oligomers or peptide  
 CC nucleic acids for analysing diseases associated with the methylation  
 CC states of the CpG dinucleotides of (I). The array is useful for  
 CC determining genetic and/or epigenetic parameters, classification,  
 CC differentiation, grading, staging, treatment and/or diagnosis of  
 CC astrocytomas, or the predisposition to astrocytomas by analysing cytosine  
 CC methylations, involves obtaining a biological sample containing genomic  
 CC DNA, extracting the genomic DNA, converting cytosine bases which are  
 CC unmethylated at the 5-position, in the genomic DNA sample, to uracil or  
 CC another base which is dissimilar to cytosine in terms of hybridisation  
 CC behaviour, by chemical treatment and amplifying chemically pre-treated  
 CC genomic DNA fragments using the array and a polymerase, where the  
 CC amplificates carry a detectable label. The method further involves  
 CC identifying methylation status of one or more cytosine positions, and  
 CC analysing methylation status of the cytosine positions by reference to  
 CC one or more data sets. The genomic DNA is chemically treated by using a  
 CC bisulphite, hydrogen sulphite or disulphite. The amplification step  
 CC amplifies DNA which is of particular interest in astrocytoma or brain  
 CC tissue, based on the specific genomic methylation status of brain  
 CC tissues, as opposed to background DNA. The amplificates carry a  
 CC fluorescent label or radionuclide. Optionally, the labels of the  
 CC amplificates are detachable molecule fragments having a typical mass  
 CC which are detected in a mass spectrometer. The fragments of chemically  
 CC pre-treated genomic DNA to be amplified, have a single positive or  
 CC negative charge for a better detectability in the mass spectrometer.  
 CC Preferably, the amplificates or fragments of the amplificates are  
 CC detected by matrix assisted laser desorption/ionization mass spectrometry  
 CC (MALDI) or using electron spray mass spectrometry (ESI). The present  
 CC sequence is one of the chemically pre-treated reference DNA samples of  
 CC the invention. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 8666 BP; 2444 A; 168 C; 1868 G; 4186 T; 0 U; 0 Other;  
 Query Match 15.2%; Score 106.6; DB 6; Length 8666;  
 Best Local Similarity 49.0%; Pred. No. 2.9e-09;  
 Matches 312; Conservative 0; Mismatches 324; Indels 1; Gaps 1;  
 QY 12 AAAGTTTTTTTTTTTTCATGATTTTATAAAATACATTTCTTTTATTATTATTAT 71  
 Db 1547 AAAAGTTTTTTTATTATTAAATTTTATTATATATATTTTAAATTTTATTATT 1606  
 QY 72 ACTTTTAAAGTTTGGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGT 131

Db 1607 TATTTTAAAGTTTTCAGAGTATATGTGTATAAATGTGTAGGTTTGTATATATATATATGT 1666  
 QY 132 GCCATGCTGGTGTGCTGCACCCATTAACATCAATGAAGTTTTTTTTTAAATTTTAGTGACA 191  
 Db 1667 GTTATGTTGGTGTGTTGTTATTTAAATTTA-TTATTTAGTATTAGGTATATTTTTTAAT 1725  
 QY 192 GTTTTAGTCATTTTCTTAATTTGAAAGTATCATAAGTAATCCATAAATTTTGAAAAAATGT 251  
 Db 1726 GTTATTTTTTTTTTTTTTTTTTTTATATAAGATTTTAAATGGATAATGGATTTTAAATTTT 1785  
 QY 252 TAACTACTCTGATAAAAAAGTTTTTATAGTTTCTACTTTTAAAGCAAAATTTCCATAGGGCA 311  
 Db 1786 AGAGTAAATGGTTTTTATTAAAGATGTTATAATTTTTTTAGAGTTTTTATGTAAATAT 1845  
 QY 312 TGGTAATGTAGTTTCAACATTACTTTGCAGTTTCAGTTTAGTAAATAAATATTAAAGCCTAG 371  
 Db 1846 GAGATATATATATTTAAAAATTTGTTTTCGTATTTTAAAGTAGTTAAATTTTATATTTT 1905  
 QY 372 TAAGTATATAATTTAATTTGTCAAATAATTTGGAAATACCATGGGTACTTAATTTGATTTT 431  
 Db 1906 TTTATAATGTTATTAAATGTTGTTTTATATGTTGTTATTTTATTTTATTTTATTAAATA 1965  
 QY 432 ACCAAATTTCCATGGAAACAAAGGTTGGCTATTTTTTGGATTGTATTTTTTCAATAACT 491  
 Db 1966 GTTATATATATTTTATTAAGAGTTGAAGAGTTTTTGTAGTAGGAATTTATCGTAGAGT 2025  
 QY 492 AGTACAGGAATATCATTTGTTAGTTGTAATTTTACCCCTAGAACAAACAAATGGAGTTTAGAT 551  
 Db 2026 TTTAGAGAAATTTTGAATTTTATTTGAAAGTTTTTATTAGAAATATATATGTAGTGAATA 2085  
 QY 552 AGCTAAAGTATATTTTATTTGTCATTTAATAATGTTATGAGTTAGGGCTATGATAATTA 611  
 Db 2086 TATTTTTTTTAAAAAAATTTATTTATTTTATTTTGTAGAGAGGTTATTTTATTTT 2145  
 QY 612 GTGAAACACCCCAAGAAATGTTTATATCTTTTAAATTT 648  
 Db 2146 ATAGATTTTGAAGGAGTTATTTTATTTTATTTT 2182  
 RESULT 10  
 ABQ67177  
 ID ABQ67177 standard; DNA; 8666 BP.  
 XX AC ABQ67177;  
 XX DT 28-AUG-2002 (first entry)  
 XX DE Human angiogenesis associated polynucleotide SEQ ID NO 207.  
 XX KW Human; angiogenesis; methylation; eye disease; glaucoma; tumour;  
 XX KW inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds;  
 XX KW macular degeneration; inflammatory bowel disease; Crohn's disease;  
 XX KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;  
 XX KW antiarteriosclerotic; ds.  
 XX OS Homo sapiens.  
 XX FN WO200246454-A2.  
 XX PD 13-JUN-2002.  
 XX PF 06-DEC-2001; 2001WO-EP014320.  
 XX PR 06-DEC-2000; 2000DE-01061338.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX PI Schacht O;  
 XX DR WPI; 2002-500450/53.  
 XX PT New nucleic acid fragments from chemically treated angiogenesis-

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 06:56:58 ; Search time 192 Seconds  
(without alignments)

6821.751 Million cell updates/sec

Title: US-10-661-966-1\_146001-146700\_Al46311

Perfect score: 700

Sequence: 1 cgtgttcacataaagtgtttt.....gccttttagtgatgtggca 700

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 70 summaries

Database :

Issued Patents\_NA:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*

9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*

10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112.2	16.0	601	3	US-09-949-016-77443 Sequence 77443, A
2	112.2	16.0	154626	3	US-09-949-016-14000 Sequence 14000, A
3	106.8	15.3	8766	5	US-09-984-429-354 Sequence 354, App
C 4	104.2	14.9	42595	5	US-09-984-429-469 Sequence 469, App
C 5	104	14.9	601	3	US-09-949-016-134975 Sequence 134975, A
6	104	14.9	256171	3	US-09-949-016-12822 Sequence 12822, A
7	104	14.9	256176	3	US-09-949-016-15524 Sequence 15524, A
C 8	103.8	14.8	86980	3	US-09-949-016-15344 Sequence 15344, A
C 9	102.8	14.7	260247	3	US-09-949-016-13358 Sequence 13358, A
C 10	102.6	14.7	601	3	US-09-949-002-2044 Sequence 2044, App
C 11	102.6	14.7	601	3	US-09-949-002-2045 Sequence 2045, App
C 12	102.6	14.7	18999	3	US-09-949-002-703 Sequence 703, App
C 13	102.6	14.7	26225	5	US-09-984-429-448 Sequence 448, App
C 14	102.6	14.7	27271	3	US-09-949-002-622 Sequence 622, App
C 15	102.6	14.7	360470	3	US-09-949-016-13173 Sequence 13173, A
C 16	102.4	14.6	21597	5	US-09-984-429-309 Sequence 309, App
17	102.4	14.6	194889	3	US-09-949-016-15654 Sequence 15654, A
18	101.4	14.5	325	3	US-09-513-999C-18942 Sequence 18942, A
19	101.2	14.5	69924	3	US-09-949-016-15367 Sequence 15367, A
20	101	14.4	363032	3	US-09-949-016-12415 Sequence 12415, A
21	101	14.4	363033	3	US-09-949-016-15754 Sequence 15754, A
22	100.8	14.4	181251	3	US-09-949-016-15970 Sequence 15970, A
C 23	100.8	14.4	193169	3	US-09-949-016-15091 Sequence 15091, A

ALIGNMENTS

RESULT 1

US-09-949-016-77443

; Sequence 77443, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 77443

; LENGTH: 601

Sequence 426, App  
Sequence 454, App  
Sequence 15703, A  
Sequence 16066, A  
Sequence 150430, A  
Sequence 13420, A  
Sequence 12611, A  
Sequence 14413, A  
Sequence 15473, A  
Sequence 13404, A  
Sequence 16065, A  
Sequence 16, Appl  
Sequence 16, Appl  
Sequence 16, Appl  
Sequence 13276, A  
Sequence 14374, A  
Sequence 550, App  
Sequence 455, App  
Sequence 429, App  
Sequence 15744, A  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 12614, A  
Sequence 13027, A  
Sequence 14577, A  
Sequence 14578, A  
Sequence 59509, A  
Sequence 59510, A  
Sequence 360, App  
Sequence 32, Appl  
Sequence 38, Appl  
Sequence 13828, A  
Sequence 1542, App  
Sequence 13730, A  
Sequence 11820, A  
Sequence 17182, A  
Sequence 15419, A  
Sequence 13477, A  
Sequence 398, App  
Sequence 16151, A  
Sequence 59511, A  
Sequence 179319, A  
Sequence 468, App  
Sequence 16065, A  
Sequence 13675, A  
Sequence 12386, A

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; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-77443

Query Match      16.0%; Score 112.2; DB 3; Length 601;
Best Local Similarity 84.6%; Pred. No. 3.9e-13;
Matches 126; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 13 AAGTTTTTTTTTTTGTGATGATTTTAAATAAATATCAATTTCTTTTTTATATATATATA 72
Db 298 AACTTTTTTTTTTTTGTGCTGGAAATCTTTTTTTTTTTTAAATTTATATATATATA 357

QY 73 CTTTAAAGTTTTTAGGGTACATGTCGAAAGTGTGCAGGTAGTTACATATATATACATGTG 132
Db 358 CTTTAAAGTTTTTAGGGTACATGTCGCAACGTCGAGGTGTTGTACATATGTATACATGTG 417

QY 133 CCATGCTGGTGTGCTGCACCCCACTTAATCT 161
Db 418 CCATGTTGGTGTGCTGCACCCCACTTAATCT 446

RESULT 2
US-09-949-016-14000
; Sequence 14000, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14000
; LENGTH: 154626
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(154626)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14000

Query Match      16.0%; Score 112.2; DB 3; Length 154626;
Best Local Similarity 84.6%; Pred. No. 4.9e-13;
Matches 126; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 13 AAGTTTTTTTTTTTGTGATGATTTTAAATAAATCAATTTCTTTTTTATATATATATA 72
Db 133339 AACTTTTTTTTTTTTGTGCTGGAAATCTTTTTTTTTTTTAAATTTATATATATA 133398

QY 73 CTTTAAAGTTTTTAGGGTACATGTCGAAAGTGTGCAGGTAGTTACATATATATACATGTG 132
Db 133399 CTTTAAAGTTTTTAGGGTACATGTCGCAACGTCGAGGTGTTGTACATATGTATACATGTG 133458

QY 133 CCATGCTGGTGTGCTGCACCCCACTTAATCT 161
Db 133459 CCATGTTGGTGTGCTGCACCCCACTTAATCT 133487

RESULT 3
US-09-984-429-354
; Sequence 354, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
```

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; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 354
; LENGTH: 8766
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-354

Query Match      15.3%; Score 106.8; DB 5; Length 8766;
Best Local Similarity 94.1%; Pred. No. 4.8e-12;
Matches 111; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 44 TATCATTTTCTTTTTTATTATTATTATATATCTTTTAAAGTTTATAGGTACATGTGCAAGTG 103
Db 2 TTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 61

QY 104 TGCAGGTAGTTACATATATATATACATGTGCCATGCTGCTGGTGTGTCGCCCACTTAATCT 161
Db 62 TGCAGGTAGTTACATATATATATATACATGTGCCATGCTGCTGGTATGCTGCCCACTTAATCT 119

RESULT 4
US-09-984-429-469/c
; Sequence 469, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 469
; LENGTH: 42595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7234)..(7234)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-984-429-469

Query Match      14.9%; Score 104.2; DB 5; Length 42595;
Best Local Similarity 86.9%; Pred. No. 1.6e-11;
Matches 126; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 17 TTTTCTTTTTCATCATTTTAAATAAATATCATCTTCTTTTATTATTATTATTACTTT 76
Db 18952 TCTTTTCTTTTAAATTAATTTTAAATTTTATTATTATTATTATTATTATTATAC-TT 18894

QY 77 TAAAGTTTATAGGTACATGTGCACAAAGTGCAGGTTAGTTACATATATATACATGTGCCAT 136
Db 18893 TAAAGTTTATAGGTACATGTGCACATTTGTCAGGTTAGTTACATATGTATACATGTGCCAT 18834

QY 137 GCTGTGTGCTGCACCCCAATTAATCT 161
Db 18833 GCTGTGTGCTGCACCCCAATTAATCT 18809

RESULT 5
US-09-949-016-134975/c
; Sequence 134975, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134975
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-134975

Query Match      14.9%; Score 104; DB 3; Length 601;
Best Local Similarity 82.6%; Pred. No. 1.5e-11;
Matches 119; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 18 TTTTCTTTTTCATGATTTTAAATAAATATCATCTTCTTTTATTATTATTACTTTT 77
Db 290 TTATATACTTTTGCCCACTGTATAAATCTCTTATTCTTTTTCATTATTATTACTTTT 231

QY 78 AAGTTTATAGGTACATGTGCACAAAGTGCAGGTTAGTTACATATATACATGTGCCATG 137
Db 230 AAGTTTATAGGTACATGTGCACAAATGTGCAGGTTAGTTACATATGTATACATGTGCCATG 171

QY 138 CTGGTGTGCTGCACCCCAATTAATCT 161
Db 170 CTGGTGTGCTGCACCCCAATTAATCT 147

RESULT 6
US-09-949-016-12822
; Sequence 12822, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12822
; LENGTH: 256176
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(256176)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12822

Query Match      14.9%; Score 104; DB 3; Length 256176;
Best Local Similarity 82.6%; Pred. No. 1.9e-11;
Matches 119; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 18 TTTTCTTTTTCATGATTTTAAATAAATATCATCTTCTTTTATTATTATTACTTTT 77
Db 89281 TTATATACTTTGTTGCCATCTGTATAATCTCTTATTCTTTTTCATTATTATTACTTTT 89340

QY 78 AAGTTTATAGGTACATGTGCACAAAGTGCAGGTTAGTTACATATATACATGTGCCATG 137
Db 89341 AAGTTTATAGGTACATGTGCACAAATGTGCAGGTTAGTTACATATGTATACATGTGCCATG 89400

QY 138 CTGGTGTGCTGCACCCCAATTAATCT 161
Db 89401 CTGGTGTGCTGCACCCCAATTAATCT 89424

RESULT 7
US-09-949-016-15524
; Sequence 15524, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15524
; LENGTH: 256176
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(256176)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15524

Query Match      14.9%; Score 104; DB 3; Length 256176;
Best Local Similarity 82.6%; Pred. No. 1.9e-11;
Matches 119; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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Db 107969 TAC-TTTAAGTTTATAGGGTACATGTGCACATGTGCAGGTTAGTTACATATGTATACATG 108027
QY 131 TGCCATGCTGGTGTGCTGCACCCATTAACTC-ACATGAGTTTATTTTAAATTTTAGTGA 189
Db 108028 TGCCATGCTGTGCACGTGCACCCACTCACTGTCACTAGCATTAATTTTAAATTTGTTTA 108087
QY 190 CAGTTTATAGTCA 201
Db 108088 GTTTTTTTTGA 108099

RESULT 18
US-09-513-999C-18942
; Sequence 18942, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 6783961
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 18942
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 124.
; OTHER INFORMATION: w=a or t
; NAME/KEY: misc_feature
; LOCATION: 127
; OTHER INFORMATION: w=a or t
; NAME/KEY: misc_feature
; LOCATION: 130
; OTHER INFORMATION: w=a or t
; NAME/KEY: misc_feature
; LOCATION: 143
; OTHER INFORMATION: m=a or c
; NAME/KEY: misc_feature
; LOCATION: 151
; OTHER INFORMATION: w=a or t
; NAME/KEY: misc_feature
; LOCATION: 308
; OTHER INFORMATION: n=a, g, c or t
; NAME/KEY: misc_feature
; LOCATION: 309
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-18942

Query Match 14.5%; Score 101.4; DB 3; Length 325;
Best Local Similarity 83.7%; Pred. No. 4.6e-11;
Matches 108; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 33 TTTTAATAAATATACATTTCTTTTTTATTATTATTATTTTAAAGTTTATAGGGTACA 92
Db 86 TTTTATTATGTTTAACTTTTTTTTATTATTATTATTAAATTTWAAGTTTATAGGTACA 145

QY 93 TGTGCAAGTGTGCAGGTTAGTTACATATATACATGTGCATGCTGGTGTGTCAC 152
Db 146 TGTGCWCAATGTCAGGTTAGTTACATATGTATACATGTGCATGCTGGTGTGTCAC 205
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QY 153 CATTAACCTC 161
Db 206 CATTAACCTC 214
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RESULT 19
US-09-949-016-15367
; Sequence 15367, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15367
; LENGTH: 69924
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15367

Query Match 14.5%; Score 101.2; DB 3; Length 69924;
Best Local Similarity 81.6%; Pred. No. 6.3e-11;
Matches 129; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

QY 4 TTTCCACATAAAGTTTTTTTTTTTCATGATTTTAAATAAAATATCATTTCTTTTTTATT 63
Db 49733 TTTAGTTTATAGCTTGTAACTTCATTTATTTTATTTTATTTTATTTTATTTATT 49792

QY 64 ATTATTATACCTTTTAAGTTTTCAGGTACATGTCACCAAGTGCAGGTAGTTACATATAT 123
Db 49793 ATTATTATACCTTT-AAAGTTTTCAGGTACATGTCACCAATGTCAGGTAGTTACATATGT 49851

QY 124 ATACATGTGCCATGCTGCTGTGCTGCACCCCACTTAACCTC 161
Db 49852 ATACATGTGCCATGCTGCTGTGCTGCACCCCACTTAACCTC 49889
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RESULT 20
US-09-949-016-12415
; Sequence 12415, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12415
; LENGTH: 363032
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)...(363032)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12415

Query Match      14.4%; Score 101; DB 3; Length 363032;
Best Local Similarity 79.9%; Pred. No. 7.3e-11;
Matches 119; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 14 AGTTTTTTTTTTGATGATTTTAAATAAATATCATTTCTTTTTTATTATTATTATAC 73
Db 76601 AATTTTTTTTTTTGTCGCTGGAATTTCTTTTTTTTTTTTTTTTTTAAATTATA 76660

QY 74 TTTTAAGTTTTAGGTCATGTGCAGAGTTAGTACATATATATACATGTGC 133
Db 76661 CTTTAAAGTTTTAGGTCATGTGCAGAGTTAGTACATATGTATACATGTGC 76720

QY 134 CATGCTGGTGTGCTGCCACCCCAATTAAC 162
Db 76721 CATGCTGGTGTGCTGCCACCCCACTAACTCA 76749

RESULT 21
US-09-949-016-15754
; Sequence 15754, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15754
; LENGTH: 363033
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(363033)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15754

Query Match      14.4%; Score 101; DB 3; Length 363033;
Best Local Similarity 79.9%; Pred. No. 7.3e-11;
Matches 119; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 14 AGTTTTTTTTTTGATGATTTTAAATAAATATCATTTCTTTTTTATTATTATTATAC 73
Db 76601 AATTTTTTTTTTTGTCGCTGGAATTTCTTTTTTTTTTTTTTTTTTAAATTATA 76660

QY 74 TTTTAAGTTTTAGGTCATGTGCAGAGTTAGTACATATATATACATGTGC 133
Db 76661 CTTTAAAGTTTTAGGTCATGTGCAGAGTTAGTACATATGTATACATGTGC 76720

QY 134 CATGCTGGTGTGCTGCCACCCCAATTAAC 162
Db 76721 CATGCTGGTGTGCTGCCACCCCACTAACTCA 76749

RESULT 22
US-09-949-016-15970
; Sequence 15970, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15970
; LENGTH: 181251
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(193169)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15970

Query Match      14.4%; Score 100.8; DB 3; Length 181251;
Best Local Similarity 64.5%; Pred. No. 7.8e-11;
Matches 182; Conservative 0; Mismatches 97; Indels 3; Gaps 2;

QY 16 TTTTTTTTTTTGATGATTTTAAATAAATATCATTTCTTTTTTATTATTATTACTT 75
Db 75583 TTCTTTTTTTTATTATTAAAGTTTTTTTAAAAATTTATTAGTATTATTATTAC-T 75641

QY 76 TTAAGTTTTAGGTCATGTGCAGAGTTAGTACATATATATACATGTGCCA 135
Db 75642 TTAAGTTTTAGGTCATGTGCAGAGTTAGTACATATGTATACATGTGCCA 75701

QY 136 TGCTGGTGTGCTGCCACCCCAATTAACATGAGTTTTTTTAAATTTTAGTCACAGTTT 195
Db 75702 TGCTGGTGTGCTGCCACCCCAATGAGGAGCATGGAATGGAATGGAATCATCTCTACTA 75761

QY 196 TAGTCATTTTCTTAATGAAAGTATCATTAAGTAATCCATAAATTTGAAAAAATGTTAAC 255
Db 75762 AACTCGTTTTTGTCTTCTAAAGAAT--TTAGGACATGTTATTTTGGAGACTGTTTTTACA 75819

QY 256 TACTCTGATAAAAAAGTTTTTATAGTTTCTCTACTTTTAAAGCAA 297
Db 75820 TTTGATTATGGATGCATTTTAGTTGTTTAAATCTTTGGCTA 75861

RESULT 23
US-09-949-016-15091/c
; Sequence 15091, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15091
; LENGTH: 193169
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(193169)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15091
```

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Query Match      14.4%; Score 100.8; DB 3; Length 193169;
Best Local Similarity 81.2%; Pred. No. 7.8e-11;
Matches 117; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 19 TTTTITTTTGATGATTTTAATAAAATATACATTTCTTTTATTTATTTATTTATTTATTTA 78
DB 21017 TTATTGTTTGTGTTGTTTTTACCGTATTACTATTCTTTTTTTTTTTTATATCTTTTA 20958

QY 79 AGTTTITAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCGCATGC 138
DB 20957 AGTTTITAGGTACATGTGCAACGTCGAGGTTGTTACATATATATACATGTGCGCATGT 20898

QY 139 TGGTGTGTGCACCACTAACTCA 162
DB 20897 TGGTGTGTGTACCCATTAACCTCA 20874

RESULT 24
US-09-984-429-426/c
; Sequence 426, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: PZ018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 426
; LENGTH: 1055
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-426

Query Match      14.3%; Score 100.4; DB 5; Length 1055;
Best Local Similarity 84.9%; Pred. No. 7.5e-11;
Matches 124; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 16 TTTTITTTTGTGATGATTTTAATAAAATATACATTTCTTTTATTTATTTATTTATTTACTT 75
DB 1038 TTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATAC-T 980

QY 76 TTAAGTTTITAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135
DB 979 TTAAGTTTITAGGTACATGTGCAACATGTGCAGGTTAGTGACATGTGTATACATGTGCCA 920

QY 136 TGCTGGTGTGCTGCACCCATTAACCTC 161
DB 919 TGCTGGTGTGCTGCACCCATTAACCTC 894

RESULT 26
US-09-949-016-15703/c
; Sequence 15703, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15703
; LENGTH: 91538
; TYPE: DNA
; ORGANISM: Human
US-09-984-429-426/c
; Sequence 426, Application US/09984429
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US-09-949-016-15703
Query Match      14.3%; Score 100.4; DB 3; Length 91538;
Best Local Similarity 84.9%; Pred. No. 9e-11;
Matches 124; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 16 TTTTCTTTTTCGATGATTTTAAATAAATATCATTTCTTTTATTATTATATATACTT 75
Db 23790 TTTATTATTATTAAATTTTATTATTATTATTATTATTATTATTATTATTATAC-T 23732

QY 76 TTAAGTTTTAGGGTACATGTGCAAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 135
Db 23731 TTAAGTTTTAGGGTACATGTGCACATGTGCAGGTAGTTACATATGTATACATGTGCCA 23672

QY 136 TGCTGTGTGCTGCACCCATTAACCT 161
Db 23671 TGCTGTGTGCTGCACCCACTAATCT 23646

RESULT 27
US-09-949-016-16066/c
; Sequence 16066, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16066
; LENGTH: 144362
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(144362)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16066

Query Match      14.3%; Score 100.4; DB 3; Length 144362;
Best Local Similarity 82.5%; Pred. No. 9.2e-11;
Matches 127; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

QY 9 CATAAAGTTTTTTTTTTCGATGATTTTAAATAAATATCATTTCTTTTATTATTAT 68
Db 26372 CAGAAGCTCTCTTTATTATTATTATGATGATGATGATTTATTATTATTATTAT 26313

QY 69 TATACTTTTAAGTTTAAAGGTACATGTGCAAAAGTGTGCAGGTAGTTACATATATACA 128
Db 26312 TATAC-TTTAAGTTTAAAGGTACATGTGCACAAATGTGCAGGTAGTTACATATGATACA 26254

QY 129 TGTGCCATGCTGGTGTCTGCACCCATTAACCTCA 162
Db 26253 TGTGCCATGCTGGTGTCTGCACCCACTAATCTCA 26220

RESULT 28
US-09-949-016-150430
; Sequence 150430, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 150430
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(47363)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13420

Query Match      14.3%; Score 100.2; DB 3; Length 47363;
Best Local Similarity 81.5%; Pred. No. 9.6e-11;
Matches 128; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

QY 5 TTCACATAAAGTTTTTTTTTTTTCGATGATTTTAAATAAATATCATTTCTTTTATTATTA 64
Db 26253 TTCACATAAAGTTTTTTTTTTTTCGATGATTTTAAATAAATATCATTTCTTTTATTATTA 64
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Db 321248 CATTAACCTC 321256

RESULT 33
US-09-949-016-13404
; Sequence 13404, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13404
; LENGTH: 237863
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13404

Query Match 14.3%; Score 100; DB 3; Length 237863;
Best Local Similarity 80.6%; Pred. No. 1.1e-10;
Matches 129; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

Qy 2 TGTTTCACATAAGTTTTTTTTTTTTCATGATTTTAAATAAATATCATCTCTTTTCTTTTAA 61
Db 154366 TGTACATATCAGACGCTGTTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTT 154425

Qy 62 TTATTATTATCTTTTAAAGTTTGGGTACATGTGCAAGTGTGCAGGTTAGTTACATAT 121
Db 154426 TTATTATTATGCTTTTAAAGTTTGGGTACATGTGCAAGTGTGCAGGTTAGTTACATAT 154484

Qy 122 ATATACATGTGCCATGCTGCTGTGCTGCACCCCAATTAACCTC 161
Db 154485 GCATACATGTGCCATGCTGCTGTGCTGTACCCCAATTAACCTC 154524

RESULT 34
US-09-949-016-16065/c
; Sequence 16065, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16065
; LENGTH: 212139
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16065

Query Match 14.3%; Score 99.8; DB 3; Length 212139;
Best Local Similarity 81.1%; Pred. No. 1.2e-10;
Matches 116; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 18 TTTTCTTTTGGATGATTTTAAATAAATATCATCTTCTTTTCTTTTCTTTTCTTTTCTTTT 77
Db 125374 TTATCTACTTGATAGCTCCACTTGGATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 125315

Qy 78 AAGTTTTCAGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATATATATACATGTGCCATG 137
Db 125314 AAGTTTTCAGGTACATGTGCAACACGTCGCAACTTTGTTACATATGTATACATGTGCCA 125255

Qy 138 CTGGTGTGCTGCACCCCAATTAACCT 160
Db 125254 TTGGTATGCTGCACCCCAATTAACCT 125232

RESULT 35
US-09-245-041-16/c
; Sequence 16, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; OF BODY WEIGHT DISORDERS INCLUDING OBESITY
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/093,630
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/104,978
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 4072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-245-041-16

Query Match 14.2%; Score 99.6; DB 3; Length 4072;
Best Local Similarity 80.1%; Pred. No. 1.1e-10;
Matches 117; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 16 TTTTCTTTTTCATGATTTTAAATAAATATCATCTTCTTTTCTTTTCTTTTCTTTTCTTTT 75
Db 4066 TTTTCTTTTTCATGATTTTAAATAAATATCATCTTCTTTTCTTTTCTTTTCTTTTCTTTT 4007

Qy 76 TTAAGTTTTCAGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATATATACATGTGCCA 135
Db 4006 TTAAGTTTTCAGGTACATGTGCACACATGCAGGTTGTTACATATGTATACATATGCCA 3947

Qy 136 TGCTGTGCTGCACCCCAATTAACCTC 161
Db 3946 TGTGTGTGCTGCACCCCAATTAACCTC 3921

RESULT 36
US-09-358-055B-16/c
; Sequence 16, Application US/09358055B
; Patent No. 6713277
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D. L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
; TREATMENT OF BODY WEIGHT DISORDERS INCLUDING
; OBESITY
; FILE REFERENCE: 7853-151
; CURRENT APPLICATION NUMBER: US/09/358,055B
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
```



```
; LENGTH: 4072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-358-055B-16

Query Match      14.2%; Score 99.6; DB 3; Length 4072;
Best Local Similarity 80.1%; Pred. No. 1.1e-10;
Matches 117; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGTGATGATTTTAATAAATATACATTTCTTTTATTTATTTATTTACTT 75
Db 4066 TTTTCTTTTGTGATGATTTTAATAAATATACATTTCTTTTATTTATTTATTTACT 4007

QY 76 TTAAGTTTATAGGGTACATGTCGCAAGTGTGACAGGTTAGTTACATATATATACATGTGCCA 135
Db 4006 TTAAGTTTATAGGGTACATGTCGCAACATGCGAGGTTTGTACATATGTATACATATGCCA 3947

QY 136 TGCTGGTGTGTCGACCCCAATTAACTC 161
Db 3946 TGTGGTGTGTCGACCCCAATTAACTC 3921

RESULT 37
US-09-893-238-16/c
; Sequence 16, Application US/09893238
; Patent No. 6727348
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagie, D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; FILE REFERENCE: 7853-237
; CURRENT APPLICATION NUMBER: US/09/893,238
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/093,630
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: 60/104,978
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 4072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-893-238-16

Query Match      14.2%; Score 99.6; DB 3; Length 4072;
Best Local Similarity 80.1%; Pred. No. 1.1e-10;
Matches 117; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGTGATGATTTTAATAAATATACATTTCTTTTATTTATTTATTTACTT 75
Db 4066 TTTTCTTTTGTGATGATTTTAATAAATATACATTTCTTTTATTTATTTATTTACT 4007

QY 76 TTAAGTTTATAGGGTACATGTCGCAAGTGTGACAGGTTAGTTACATATATATACATGTGCCA 135
Db 4006 TTAAGTTTATAGGGTACATGTCGCAACATGCGAGGTTTGTACATATGTATACATATGCCA 3947

QY 136 TGCTGGTGTGTCGACCCCAATTAACTC 161
Db 3946 TGTGGTGTGTCGACCCCAATTAACTC 3921

RESULT 38
US-09-949-016-13276/c
; Sequence 13276, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14374
; LENGTH: 112623
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(112623)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13276

Query Match      14.2%; Score 99.6; DB 3; Length 112623;
Best Local Similarity 83.3%; Pred. No. 1.3e-10;
Matches 125; Conservative 0; Mismatches 24; Indels 1; Gaps 1;

QY 12 AAAGTTTTTTTTTTTGGATGATTTTAATAAATATATCAATTTCTTTTATTTATTTATTTAT 71
Db 12 AAAGTTTTTTTTTTTGGATGATTTTAATAAATATATCAATTTCTTTTATTTATTTATTTAT 71
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Db 4895 -TAAAGTTTGGGTACATGTGCACAAATGTGCAGGTTAGTGCACATATGTATACATGTGCCA 4837  
QY 136 TCCTGGTGTGCTGCACCCCAATTAAC 160  
Db 4836 TGCTGGTGTGCTGCACCCCAATTAAC 4812

RESULT 43  
US-09-949-016-15744  
; Sequence 15744, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15744  
; LENGTH: 64049  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15744

Query Match 14.2%; Score 99.4; DB 3; Length 64049;  
Best Local Similarity 80.1%; Pred. No. 1.4e-10;  
Matches 129; Conservative 0; Mismatches 31; Indels 1; Gaps 1;  
QY 2 TGTTCACATAAAGTTTTTTTTTTTGGATGATTTTAAATAAATATCATTTCTTTTTTTA 61  
Db 50324 TGAGTTACAAAAGTTTAACTTTTATGTTAAAGATTATTTATTTTAAATTAA 50383  
QY 62 TTATATATATCTTTTAAAGTTTTAGGTACATGTGCACAAAGTGTGCAGTTAGTTACATAT 121  
Db 50384 TTATATATATAC-TTAAAGTTTTAGGTACATGTGCACAAAGTGTGCAGTTAGTTACATAT 50442  
QY 122 ATATACATGTGCCATGCTGCTGCTGCACCACTTAAC 162  
Db 50443 GTATACATGTGCCATGCTGCTGCTGCACCACTTAAC 50483

RESULT 44  
US-09-818-512-3  
; Sequence 3, Application US/09818512  
; Patent No. 6537780  
; GENERAL INFORMATION:  
; APPLICANT: BEASLEY, Ellen et al.  
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001192  
; CURRENT APPLICATION NUMBER: US/09/818,512  
; CURRENT FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 116592  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(116592)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-818-512-3

Query Match 14.2%; Score 99.4; DB 3; Length 116592;  
Best Local Similarity 82.4%; Pred. No. 1.4e-10;  
Matches 126; Conservative 0; Mismatches 26; Indels 1; Gaps 1;  
QY 6 TCACATAAAGTTTTTTTTTTTGGATGATTTTAAATAAATATCATTTCTTTTTTATTAT 65  
Db 48471 TCAGAAAAATATATTTTTTTTTTTCATTTATTTTATTTATTTATTTATTTT 48530  
QY 66 TATTATACTTTTAAAGTTTGGGTACATGTGCACAAAGTGTGCAGTTAGTTACATATAT 125  
Db 48531 TATTATACTC-TAAGTTTGGGTACATGTGCACATTTGTGCAGGTTAGTTACATATGTAT 48589  
QY 126 ACATGTGCCATGCTGGTGTGCTGCACCCCAATTA 158  
Db 48590 ACATGTGCCATGCTGGTGTGCTGCACCCCACTAA 48622

RESULT 45  
US-10-354-065-3  
; Sequence 3, Application US/10354065  
; Patent No. 6884609  
; GENERAL INFORMATION:  
; APPLICANT: BEASLEY, Ellen et al.  
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001192DIV  
; CURRENT APPLICATION NUMBER: US/10/354,065  
; CURRENT FILING DATE: 2003-01-30  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 116592  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(116592)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-354-065-3

Query Match 14.2%; Score 99.4; DB 3; Length 116592;  
Best Local Similarity 82.4%; Pred. No. 1.4e-10;  
Matches 126; Conservative 0; Mismatches 26; Indels 1; Gaps 1;  
QY 6 TCACATAAAGTTTTTTTTTTTGGATGATTTTAAATAAATATCATTTCTTTTTTATTAT 65  
Db 48471 TCAGAAAAATATATTTTTTTTTTTCATTTATTTTATTTATTTATTTT 48530  
QY 66 TATTATACTTTTAAAGTTTGGGTACATGTGCACAAAGTGTGCAGTTAGTTACATATAT 125  
Db 48531 TATTATACTC-TAAGTTTGGGTACATGTGCACATTTGTGCAGGTTAGTTACATATGTAT 48589  
QY 126 ACATGTGCCATGCTGGTGTGCTGCACCCCAATTA 158  
Db 48590 ACATGTGCCATGCTGGTGTGCTGCACCCCACTAA 48622

RESULT 46  
US-09-949-016-12614/c  
; Sequence 12614, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
US-09-949-016-12614/c

; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 12614  
 ; LENGTH: 248968  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(248968)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-949-016-12614  
  
 Query Match 14.2%; Score 99.2; DB 3; Length 248968;  
 Best Local Similarity 86.4%; Pred. No. 1.6e-10;  
 Matches 121; Conservative 0; Mismatches 18; Indels 1; Gaps 1;  
  
 QY 22 TTTTGGTACATGTCACAAAGTGTGCAGGTTAGTTACATATATACATGTGCCATGCTGG 81  
 DB 163938 TTTTCCTTTCTTTTAAATTAATTTATTTTATTTATTTATTTATTTATTTTAACTTTTAACT 163880  
  
 QY 82 TTTAGGTCATGTGCAAAAGTGTGCAGGTTAGTTACATATATACATGTGCCATGCTGG 141  
 DB 163879 TTTAGGTCATGTGCACAAATGTGCAGGTTAGTTACATATGTATACATGTGCCATGCTGG 163820  
  
 QY 142 TGTGCTGCACCCATTAACTC 161  
 DB 163819 TGTACTGCACCCATTAACTC 163800  
  
 RESULT 47  
 US-09-949-016-16061/c  
 ; Sequence 16061, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 16061  
 ; LENGTH: 250958  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(250958)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-949-016-16061  
  
 Query Match 14.2%; Score 99.2; DB 3; Length 250958;  
 Best Local Similarity 86.4%; Pred. No. 1.6e-10;  
 Matches 121; Conservative 0; Mismatches 18; Indels 1; Gaps 1;  
  
 QY 22 TTTTGGTACATGTCACAAAGTGTGCAGGTTAGTTACATATATACATGTGCCATGCTGG 81  
 DB 213928 TTTTCCTTTCTTTTAAATTAATTTATTTTATTTATTTATTTATTTTAACTTTTAACT 213870  
  
 QY 82 TTTAGGTCATGTGCAAAAGTGTGCAGGTTAGTTACATATATACATGTGCCATGCTGG 141  
 DB 213869 TTTAGGTCATGTGCACAAATGTGCAGGTTAGTTACATATGTATACATGTGCCATGCTGG 213810



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|||||
Db 411 TTTAAGTTTGGGTACATGTCACATGTCAGGTAGTTACATATATATACATGTGCC 470
QY 135 ATGCTGGTGTGCTGCACCCCACTAACTCA 162
Db 471 ATGCTGGTGGCTGCACCCCACTAACTCA 498

RESULT 53
US-09-984-429-360/c
; Sequence 360, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 360
; LENGTH: 5323
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-360

Query Match 14.1%; Score 98.8; DB 5; Length 5323;
Best Local Similarity 84.2%; Pred. No. 1.6e-10;
Matches 123; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

QY 16 TTTTCTTTTGGTATGATTTTAAATAAATATCATTTTCTTTTATTTATTTATTTATTTACTT 75
Db 5323 TTTTCTTTTGGTATGATTTTAAATAAATATCATTTTCTTTTATTTATTTATTTATTTACTT 75

QY 76 TTAAGTTTATAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 135
Db 5264 TTAAGTTTATAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 5205

QY 136 TGTGTTGCTGCTGCACCCCACTAACTC 161
Db 5204 TGTGTTGCTGCTGCACCCCACTAACTC 5179

RESULT 54
US-09-949-001-32/c
; Sequence 32, Application US/09949001
; Patent No. 6825336
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL000789
; CURRENT APPLICATION NUMBER: US/09/949,001
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/231,323
```

```
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 66524
; TYPE: DNA
; ORGANISM: Human
US-09-949-001-32

Query Match 14.1%; Score 98.8; DB 3; Length 66524;
Best Local Similarity 78.7%; Pred. No. 1.8e-10;
Matches 118; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 11 TAAAGTTTTTTTTTTTGGATGATTTTAAATAAATATCATTTTCTTTTATTTATTTATTTA 70
Db 18278 TATTTTATTTTATTTTATTTTATTTTCAATATTTTATTTATTTATTTATTTATTT 18219

QY 71 TACTTTTAAAGTTTAAAGGTACATGTGCAAAAGTGTGCAGGTAGTTACATATATATACATG 130
Db 18218 ATACTTTAAAGTTTAAAGGTACATGTGCAAAAGTGTGCAGGTAGTTACATATATACATG 18159

QY 131 TGCCATGCTGGTGTGCTGCCACCACTAACT 160
Db 18158 TGACATGCTGGTGTGCTGCCACCACTAACT 18129

RESULT 55
US-09-949-001-38/c
; Sequence 38, Application US/09949001
; Patent No. 6825336
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,001
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/231,323
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 66525
; TYPE: DNA
; ORGANISM: Human
US-09-949-001-38

Query Match 14.1%; Score 98.8; DB 3; Length 66525;
Best Local Similarity 78.7%; Pred. No. 1.8e-10;
Matches 118; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 11 TAAAGTTTTTTTTTTTGGATGATTTTAAATAAATATCATTTTCTTTTATTTATTTATTTA 70
Db 18278 TATTTTATTTTATTTTATTTTATTTTCAATATTTTATTTATTTATTTATTTATTT 18219

QY 71 TACTTTTAAAGTTTAAAGGTACATGTGCAAAAGTGTGCAGGTAGTTACATATATATACATG 130
Db 18218 ATACTTTAAAGTTTAAAGGTACATGTGCAAAAGTGTGCAGGTAGTTACATATATACATG 18159

QY 131 TGCCATGCTGGTGTGCTGCCACCACTAACT 160
Db 18158 TGACATGCTGGTGTGCTGCCACCACTAACT 18129

RESULT 56
US-09-949-016-13828/c
; Sequence 13828, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

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; CURRENT APPLICATION NUMBER: US/09/949, 016
;
; CURRENT FILING DATE: 2000-04-14
;
; PRIOR APPLICATION NUMBER: 60/241,755
;
; PRIOR FILING DATE: 2000-10-20
;
; PRIOR APPLICATION NUMBER: 60/237,768
;
; PRIOR FILING DATE: 2000-10-03
;
; PRIOR APPLICATION NUMBER: 60/231,498
;
; PRIOR FILING DATE: 2000-09-08
;
; NUMBER OF SEQ ID NOS: 207012
;
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 13828
;
; LENGTH: 87323
;
; TYPE: DNA
;
; ORGANISM: Human
;
; US-09-949-016-13828

```

	Query Match	14.1%	Score 98.8	DB 3	Length 87323	
	Best Local Similarity	78.7%	Pred. No. 1.8e-10			
	Matches 118	Conservative 0	Mismatches 32	Indels 0	Gaps 0	
Qy	12	AAAGTTTTTTTTTTTGATGATTTTAAATAAATATCAATTTCTTTTTTATATATATATAT 71				
Db	67252	AAAGATGTTTTTGTGTTTAAAGATTATAAATGCTCTTTTTTAAAAATTTTTTATTTTATTA 67193				
Qy	72	ACTTTTAAAGTTTTTAGGGTACATGTCAAAGTGTGCAGGTTAGTTACATATATATACATGT 131				
Db	67192	TACTTTTAAAGTTTTTAGGGTACATGTCACAATGTGCAGGTTAGTTACATATGTATACATGT 67133				
Qy	132	GCCATGCTGGTGTGCTGCACCCATTAACTC 161				
Db	67132	GCCATGCTGGTGTGCTGCACCCATTAACTC 67103				

```

RESULT 57
US-09-880-107-1542
; Sequence 1542, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1542
; LENGTH: 110096
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. 6974667 AD000092
US-09-880-107-1542

```

	Query Match	14.1%;	Score 98.8;	DB 4;	Length 110096;
	Best Local Similarity	84.2%;	Pred. No. 1.9e-10;		
	Matches 123;	Conservative 0;	Mismatches 22;	Indels 1;	Gaps 1;
QY	16	TTTTTTTTTTTGATGATTTTAAATAAAATACATTTCTTTTTTATATATTATATACTT	75		
Db	104835	TTTTTTTTTTTTTTTGCCCTCAAAAGTTTATTTATTTATTTATTTATTTATATAC-T	104893		
QY	76	TTAAGTTTTTAGGGTACATGTGCACAAAGTGTGACAGGTAGTTACATATATACATGTGCCA	135		
Db	104894	TTAAGTTTTTAGGGTACTTGTGCACAACTGTGACAGGTGTGTACATATGATACATGTGCCA	104953		
QY	136	TGCTGGTGTGCTGCACCCCAATTAACTC	161		

```
DB      104954   TGTGGTGCTGTCACCAATTAAGTC    104979
|||||
|||
RESULT 58
US-09-949-016-13730/c
; Sequence 13730, Application US/O9949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN G
; TITLE OF INVENTION: WITH HUMAN DISEASE, MET
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13730
; LENGTH: 163181
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(163181)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13730
```

	Query Match	14.1%	Score 98.8;	DB 3;	Length 163181;
	Best Local Similarity	84.2%;	Pred. No. 1.9e-10;		
	Matches 123;	Conservative 0;	Mismatches 22;	Indels 1;	Gaps 1;
Qy	16	TTTTTTTTTTTTTGATGATTTTTTAATAAATAATACATTTCTTTTTTATTATTATTATTACTTT	75		
Db	48276	TTGTTTTGTTTTTGCTTTTTTTTGTTGTTTTTTTATTATTATTATTACTATAC-T	48218		
Qy	76	TTAAGTTTTAGGGTACATGTGCAAAGTGTGCAGGTAGTTACATATATATACATGTGCCA	135		
Db	48217	TTAAGTTTTAGGGTACACGTGCACAAATGTGCAGGTAGTTACATATGTATACATGTGCCA	48158		
Qy	136	TGCTGTGTGTCTGCACCCATTAACTC	161		
Db	48157	TGCTGTGTGTCTGCACCCATTAACTC	48132		

```

RESULT 59
US-09-949-016-11820/c
; Sequence 11820, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11820
; LENGTH: 192700
; TYPE: DNA
; ORGANISM: Human

```





Db 83021 ATGCTGGTGGCTGCACCCACTAACTCA 83048

RESULT 63

```

US-09-984-429-398/c
; Sequence 398, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: PZO18P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 398
; LENGTH: 4897
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-398

```

	Query Match	14.1%	Score 98.6;	DB 5;	Length 4897;
	Best Local Similarity	92.0%;	Pred. No. 1.8e-10;		
	Matches 104;	Conservative 0;	Mismatches 9;	Indels 0;	Gaps 0;
Qy	49	TTTTCTTTTTTATATATATATATATCTTTTAAGTTTATAGGTTACATGTCACAAAGTGTGCAG	108		
Db	4893	TTTTTTAAATGATATTATTATTATATATCTTTTAAGTTTATAGGTTACATGTCACAAAGTGTGCAG			
Qy	109	GTTAGTTACATATATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC	161		
Db	4833	GTTAGTTACATATGATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC	4781		

## RESULT 64

```

RES001 84
US-09-949-016-16151/c
; Sequence 16151, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16151
; LENGTH: 146401

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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16151

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[illegible]

## RESULT 65

```

US-09-949-016-59511
; Sequence 59511, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59511
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-59511

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	Best Local Similarity	83.1%	Pred. No. 1.8e-10		
	Matches 123	Conservative 1	Mismatches 22	Indels 2	Gaps 1
Qy	17	TTTTTTTTTTTGATGATTTTAAATAAATCATCTTCTTTTTTTTATTATTATTAT--ACT	74		
Db	278	TCTTTTTTTTTAATTAAATTAATTTATTTATTTATTTATTTATTTATTTATTATTAGAC	337		
Qy	75	TTTAAGTTTTAGGGTACATGTGCAAGTGTGACGGTTAGTTACATATATATACATGTGCC	134		
Db	338	TTTAAGTTTTAGGGTACATGTGCAAGTGTGACGGTTAGTTACATATATATACATGTGCC	397		

RESULT 66

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US-09-349-016-179319/C
; Sequence 179319, Application US/0949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016

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; SEQ ID NO 13675
; LENGTH: 235452
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(235452)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13675

Query Match      14.1%; Score 98.4; DB 3; Length 235452;
Best Local Similarity 84.7%; Pred. No. 2.3e-10;
Matches 122; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 18 TTTTCTTTTGGTGAATTTTAAATAATATCATTTCTTTTATTTATTTATTTATTTT 77
Db 96578 TTTTCTTTTGGTGAATTTTAAATAATATCATTTCTTTTATTTATTTATTTT 77

QY 78 AAGTTTATAGGTACATGTCACAAAGTGTGACGTTAGTTACATATATATACATGTCCTATG 137
Db 96637 AAGTTTATAGGTACATGTCACAAAGTGTGACGTTAGTTACATATATATACATGTCCTATG 137

QY 138 CTGGTGTGCTGCACCACTTAATCTC 161
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RESULT 70
US-09-949-016-12386/c
; Sequence 12386, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12386
; LENGTH: 263693
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12386
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Query Match      14.1%; Score 98.4; DB 3; Length 263693;
Best Local Similarity 80.0%; Pred. No. 2.3e-10;
Matches 128; Conservative 0; Mismatches 31; Indels 1; Gaps 1;

QY 2 TGTTCACATAAAGTTTCTTTTGGTACATGTCACAAAGTGTGACGTTAGTTACATAT 61
Db 96649 TTTTCTTTTGGTGAATTTTAAATAATATCATTTCTTTTATTTATTTT 61

QY 62 TTATTATTATCTTTTAAAGTTTATAGGTACATGTCACAAAGTGTGACGTTAGTTACATAT 121
Db 96589 TTATTATTATCTTTTAAAGTTTATAGGTACATGTCACAAAGTGTGACGTTAGTTACATAT 121

QY 122 ATATACATGTCGCTGGTGTGCTGCACCACTTAATCTC 161
Db 96530 GTATACATGTCGCTGGTGTGCTGCACCACTTAATCTC 96491
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Search completed: July 19, 2006, 07:08:40  
Job time : 204 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 07:08:31 ; Search time 1464 Seconds  
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5875.235 Million cell updates/sec

Title: US-10-661-966-1\_146001-146700\_A146311

Perfect score: 700

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 70 summaries

Database : Published Applications NA Main:\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
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- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
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- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
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- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	113.2	16.2	19167	3	Sequence 1, Appli
3	109.2	15.6	100364	9	Sequence 8028, Ap
c 4	107	15.3	563	6	Sequence 6776, Ap
c 5	107	15.3	563	7	Sequence 267263,
6	107	15.3	596	4	Sequence 267263,
7	107	15.3	596	5	Sequence 728921,
8	106.8	15.3	8766	3	Sequence 065A-728921
9	106.6	15.2	8666	7	Sequence 354, App
10	106.6	15.2	8666	8	Sequence 369, App
11	106.6	15.2	8666	8	Sequence 27, Appl
12	106.6	15.2	8666	8	Sequence 95, Appl
c 13	105.8	15.1	493	4	Sequence 207, App
c 14	105.8	15.1	493	4	Sequence 477191,
c 15	105.8	15.1	493	5	Sequence 065A-477191
c 16	105.8	15.1	498	6	Sequence 267266,
c 17	105.8	15.1	498	7	Sequence 267266,
					Sequence 267262,

c 18	105.8	15.1	563	7	US-10-027-632-267262	Sequence 267262,
19	105.6	15.1	70043	8	US-10-304-113-4	Sequence 4, Appli
c 20	105.4	15.1	563	6	US-10-027-632-267264	Sequence 267264,
c 21	105.4	15.1	563	6	US-10-027-632-267265	Sequence 267265,
c 22	105.4	15.1	563	7	US-10-027-632-267264	Sequence 267264,
c 23	105.4	15.1	563	7	US-10-027-632-267265	Sequence 267265,
c 24	105.4	15.1	600	6	US-10-027-632-235941	Sequence 235941,
c 25	105.4	15.1	600	6	US-10-027-632-235942	Sequence 235942,
c 26	105.4	15.1	600	6	US-10-027-632-235943	Sequence 235943,
c 27	105.4	15.1	600	6	US-10-027-632-235941	Sequence 235941,
c 28	105.4	15.1	600	7	US-10-027-632-235942	Sequence 235942,
c 29	105.4	15.1	600	7	US-10-027-632-235943	Sequence 235943,
c 30	105.4	15.1	82938	3	US-09-818-657-3	Sequence 3, Appli
c 31	105.4	15.1	82938	13	US-11-136-623-3	Sequence 3, Appli
32	105.2	15.0	989	12	US-10-301-480-578850	Sequence 578850
33	105.2	15.0	989	12	US-10-301-480-1192259	Sequence 1192259,
34	104.8	15.0	176760	15	US-11-121-086-51	Sequence 51, Appl
35	104.6	14.9	72678	8	US-10-322-281-214	Sequence 214, Appl
36	104.6	14.9	126882	10	US-10-756-149-321	Sequence 321, App
37	104.6	14.9	1790242	9	US-10-719-993-6940	Sequence 6940, Ap
c 38	104.2	14.9	599	12	US-10-301-480-564441	Sequence 564441,
c 39	104.2	14.9	599	12	US-10-301-480-1177850	Sequence 1177850,
c 40	104.2	14.9	42595	3	US-09-984-429-469	Sequence 469, App
c 41	104	14.9	127369	6	US-10-087-192-238	Sequence 238, App
42	104	14.9	171732	15	US-11-121-086-98	Sequence 98, Appl
c 43	104	14.9	191150	12	US-10-517-905-19	Sequence 19, Appl
c 44	103.8	14.8	102980	6	US-10-087-192-1330	Sequence 1330, Ap
45	103.8	14.8	103660	9	US-10-741-600-17645	Sequence 17645, A
46	103.8	14.8	103660	10	US-10-995-561-13253	Sequence 13253, A
47	103.6	14.8	987	12	US-10-301-480-577167	Sequence 577167,
48	103.6	14.8	987	12	US-10-301-480-1190576	Sequence 1190576,
c 49	103.6	14.8	368004	3	US-09-949-654-3	Sequence 3, Appli
c 50	103.4	14.8	3200	10	US-10-450-763-12101	Sequence 12101, A
c 51	103.2	14.7	24132	3	US-09-764-860-661	Sequence 661, App
c 52	103.2	14.7	24132	6	US-10-074-095-661	Sequence 661, App
c 53	103.2	14.7	24132	7	US-10-212-872-661	Sequence 661, App
c 54	103.2	14.7	118544	11	US-10-330-773-76	Sequence 76, Appl
55	103	14.7	865	12	US-10-301-480-570607	Sequence 570607,
56	103	14.7	865	12	US-10-301-480-1184016	Sequence 1184016,
c 57	103	14.7	987	12	US-10-301-480-552761	Sequence 552761,
c 58	103	14.7	987	12	US-10-301-480-1166170	Sequence 1166170,
c 59	102.8	14.7	729	6	US-10-027-632-256997	Sequence 256997,
c 60	102.8	14.7	729	6	US-10-027-632-256998	Sequence 256998,
c 61	102.8	14.7	729	7	US-10-027-632-256997	Sequence 256997,
c 62	102.8	14.7	729	7	US-10-027-632-256998	Sequence 256998,
c 63	102.8	14.7	729	12	US-10-301-480-91798	Sequence 91798, A
c 64	102.8	14.7	729	12	US-10-301-480-91799	Sequence 91799, A
c 65	102.8	14.7	729	12	US-10-301-480-705207	Sequence 705207,
c 66	102.8	14.7	729	12	US-10-301-480-705208	Sequence 705208,
c 67	102.8	14.7	277616	8	US-10-367-094-83	Sequence 83, Appl
c 68	102.6	14.7	26225	3	US-09-764-869-1276	Sequence 1276, Ap
c 69	102.6	14.7	26225	3	US-09-984-429-448	Sequence 448, App
c 70	102.6	14.7	26225	6	US-10-091-504-1276	Sequence 1276, Ap

ALIGNMENTS

RESULT 1

US-10-661-966-1  
; Sequence 1, Application US/10661966  
; Publication No. US20050277118A1  
; GENERAL INFORMATION:  
; APPLICANT: Roth, Richard B.  
; APPLICANT: Nelson, Matthew Roberts  
; APPLICANT: Braun, Andreas  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SUBJECTS AT RISK  
; TITLE OF INVENTION: OF MELANOMA AND TREATMENTS THEREOF  
; FILE REFERENCE: 524592003800  
; CURRENT APPLICATION NUMBER: US/10/661,966  
; PRIOR FILING DATE: 2003-09-11  
; PRIOR FILING DATE: 2002-09-11

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; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 60/422,344
; PRIORITY FILING DATE: 2002-10-29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 190276
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-661-966-1

Query Match      100.0%; Score 700; DB 10; Length 190276;
Best Local Similarity 99.9%; Pred. No. 4.5e-118;
Matches 699; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGTTTCACATAAAGTTTTTTTTTTTGTGATGATTTTAATAAATATACATTTCTTTTTTT 60
DB 146001 CTGTTTCACATAAAGTTTTTTTTTTTGTGATGATTTTAATAAATATACATTTCTTTTTTT 146060

QY 61 ATTATTATTATACATTTTAAGCTTTTAGGTACATGTGCAGAGTGTGCAGGTAGTTACATA 120
DB 146061 ATTATTATTATACATTTTAAGCTTTTAGGTACATGTGCAGAGTGTGCAGGTAGTTACATA 146120

QY 121 TATATACATGTGCATGCTGGTGTGCTGCACCCATTAACCTACATGCAATGATTTTAA 180
DB 146121 TATATACATGTGCATGCTGGTGTGCTGCACCCATTAACCTACATGCAATGATTTTAA 146180

QY 181 TTTTAGTGACAGTTTGTAGTCAATTTCTTAATTTGAAAGTATCATAGTAATCCATAATTT 240
DB 146181 TTTTAGTGACAGTTTGTAGTCAATTTCTTAATTTGAAAGTATCATAGTAATCCATAATTT 146240

QY 241 GAAAAAATCTTAACCTACTCGATAAAAAAGTTTTATAGTTTCTCTTTTAAAGCAAAAT 300
DB 146241 GAAAAAATCTTAACCTACTCGATAAAAAAGTTTTATAGTTTCTCTTTTAAAGCAAAAT 146300

QY 301 TCCATAGGGCATGGTAATTTAGTTTCAACATTTACATTTGCAAGTTTCAGTTAGTAAATAAT 360
DB 146301 TCCATAGGGCATGGTAATTTAGTTTCAACATTTACATTTGCAAGTTTCAGTTAGTAAATAAT 146360

QY 361 ATTAAGCCTAGTAAGTATTAATTTAATTTGTCGCAATTAATTTGGAATATACCATGGGTACT 420
DB 146361 ATTAAGCCTAGTAAGTATTAATTTAATTTGTCGCAATTAATTTGGAATATACCATGGGTACT 146420

QY 421 TAATTGATTTTACCAATTTTCCATGGGACAAACAGGTGCGCTATTTTGGATTCATAT 480
DB 146421 TAATTGATTTTACCAATTTTCCATGGGACAAACAGGTGCGCTATTTTGGATTCATAT 146480

QY 481 TTTGAAATACTAGTACAGGAATATCATTTGTTAGTTGAATTTTGTAGCTTGAAGAAACAAAT 540
DB 146481 TTTGAAATACTAGTACAGGAATATCATTTGTTAGTTGAATTTTGTAGCTTGAAGAAACAAAT 146540

QY 541 GGAGTTTAGTACGTAAGTATTAATTTTATTTGATTTAATTAATGATGAGTTAGGCG 600
DB 146541 GGAGTTTAGTACGTAAGTATTAATTTTATTTGATTTAATTAATGATGAGTTAGGCG 146600

QY 601 TATGATAATTTAGTGAACCAACCAAGAAATGTTTATATCTTTTAAATTTTAAATAATTTGAAA 660
DB 146601 TATGATAATTTAGTGAACCAACCAAGAAATGTTTATATCTTTTAAATTTTAAATAATTTGAAA 146660

QY 661 TGACACTTGGAGTAACAAATTCCTTTTGTAGGTGATGGCA 700
DB 146661 TGACACTTGGAGTAACAAATTCCTTTTGTAGGTGATGGCA 146700

RESULT 2
US-09-764-891-8028/c
; Sequence 8028, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17

Query Match      15.6%; Score 109.2; DB 9; Length 100364;
Best Local Similarity 84.2%; Pred. No. 1.4e-09;
Matches 123; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 23 TTTTTCATGATTTTAATAAAATATCATTTTCTTTTTTTTATTTATTTATATATACATTTTAA 82
DB 30826 TTCTTTTTTTTTTTTATTTTAAACTTTTAAATTTTAAATTTTATTTATATATACATTTTAA 30885

QY 83 TTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTCATGCTGGT 142
DB 30886 TTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTCATGCTGGT 30945

QY 143 GTGCTGCACCCATTAACCTACATGAA 168
DB 30946 GTGCTGCACCCATTAACCTACCCGAA 30971

RESULT 4
US-10-027-632-267263/c
; Sequence 267263, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 267263
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-267263

Query Match 15.3%; Score 107; DB 6; Length 563;
Best Local Similarity 65.8%; Pred. No. 6.5e-10;
Matches 185; Conservative 1; Mismatches 91; Indels 4; Gaps 2;

Qy 12 AAAGTTTTTTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTTATTTAT 71
Db 455 AATATTATATACATATTAAATGTTATTATTATTTCAATATTTCTTTTATTTATTTAT 396

Qy 72 ACTTTTAAAGTTTGGGTACATGTCGCAAGTGTGCAGTTAGTTACATATATACATGT 131
Db 395 AC-TTTAAGTTTGGGTACATGTCGCAATGTGCAGTTAGTTACATATGTTACATGT 337

Qy 132 GCCATGCTGGTGTGCTGCACCCATTAACCTCACTCAATGAAAGTTTTTTTAAATTTTAGTGACA 191
Db 336 GCCATGCTGGTGTGCTGCACCCATTAACTC---GTCATTTAGCATTAGGTATATCTCCTTA 280

Qy 192 GTTTTAGTCATTTTCTTAATTTGAAAGTATCATTAAGTAAATCCATAAAATTTGAAAAAATGT 251
Db 279 ATGCTATCCCTCCCTTATTAAATATTTCTTATGTCATAAATATATTATTATAAATGT 220

Qy 252 TAACACTCTCGATAAAAAAGTTTATAGTTTCCCTACTTTTA 292
Db 219 TTTCTGTTTAAATGTTATTATTCATGTTAGTGTTTTA 179

RESULT 5
US-10-027-632-267263/c
; Sequence 267263, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 267263
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-267263

Query Match 15.3%; Score 107; DB 7; Length 563;
Best Local Similarity 65.8%; Pred. No. 6.5e-10;
Matches 185; Conservative 1; Mismatches 91; Indels 4; Gaps 2;

Qy 12 AAAGTTTTTTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTTATTTAT 71
Db 455 AATATTATATACATATTAAATGTTATTATTATTTCAATATTTCTTTTATTTATTTAT 396

Qy 72 ACTTTTAAAGTTTGGGTACATGTCGCAAGTGTGCAGTTAGTTACATATATACATGT 131
Db 395 AC-TTTAAGTTTGGGTACATGTCGCAATGTGCAGTTAGTTACATATGTTACATGT 337

Qy 132 GCCATGCTGGTGTGCTGCACCCATTAACCTCACTCAATGAAAGTTTTTTTAAATTTTAGTGACA 191
Db 336 GCCATGCTGGTGTGCTGCACCCATTAACTC---GTCATTTAGCATTAGGTATATCTCCTTA 280

Qy 192 GTTTTAGTCATTTTCTTAATTTGAAAGTATCATTAAGTAAATCCATAAAATTTGAAAAAATGT 251
Db 279 ATGCTATCCCTCCCTTATTAAATATTTCTTATGTCATAAATATATTATTATAAATGT 220

Qy 252 TAACACTCTCGATAAAAAAGTTTATAGTTTCCCTACTTTTA 292
Db 219 TTTCTGTTTAAATGTTATTATTCATGTTAGTGTTTTA 179

RESULT 6
US-09-925-065A-728921
; Sequence 728921, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 728921
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-728921

Query Match 15.3%; Score 107; DB 4; Length 596;
Best Local Similarity 83.0%; Pred. No. 6.6e-10;
Matches 122; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 15 GTTTTCTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTTATTTATTTACT 74
Db 325 GTTCTCTTTTCTTTTCTTTTAAATATTTATTATTTTATTTTAAATTTATTTACT 384





Db 1667 GTTATGTTGGTGTGTTATTAATTAATTA -TTATTTAGTATTAGGTATATATTTTAAAT 1725  
Qy 192 GTTTTAGTCATTTCCCTAAATGAAGTATCATAGTAAATCCATAAAATTTGAAAAAATGT 251  
Db 1726 GTTATTTTATTTTATTTTATTAAGATTTATAAGATTTATAAGTAAATGGAATTTTAAATTTT 1785  
Qy 252 TAACCTACTCTGATAAAAAGTTTATAGTTTCCCTACTTTTAAAGCAAAATTCATAGGGCA 311  
Db 1786 AGAGTAAATGGTTTATTTAAGGATGTTATAATTTTATAGAGTTTATTTGTAAGATAT 1845  
Qy 312 TGGTAATGTAGTTTCAACATTACTTGCAGTTTCAGTTAGTAATAATAATTAAGCCCTAG 371  
Db 1846 GAGATATATATATAAAATTTGTTTGGTATTTTAAAGTAGTTAAATTTTATATTTT 1905  
Qy 372 TAAGTATAATTAATTTATTTGTCAAATAATTTGCAAAATACCATGGTACTTAATTTGATTTT 431  
Db 1906 TTTATAGTATTAATTAATTTGTTTATATGTTTATATTTTATTTTATTTTATTAATA 1965  
Qy 432 ACCAAATTCATCGAACAACAAGTTGGCTATTTTGGATTGATATTTTGAATACT 491  
Db 1966 GTTATATATATTTTATAAGATTGAAAGAGTTTTCGATCTAGCAATTTATGTTAGT 2025  
Qy 492 AGTACAGGAATATCATGTTGTAATTTAGTTGAAATTTTAGCCTTAGAAAACAATGAGTTAGAT 551  
Db 2026 TTTAGAGAAATTTTGAATTTTATTTGAAAGTTTATTTAGAAAATATATGTTGAAGTGAATA 2085  
Qy 552 AGCTAAAGTATAATTTATTTGCTGATTTAATAATGATGATGAGTTAGGGCTATGATAATTA 611  
Db 2086 TATTTTATTTTAAAAAATTAATTTATTTTATTTTATTTTATTTTATTTTATTTT 2145  
Qy 612 GTGAAAACACCCCAAGAATGTTTATACCTTTTAAATTT 648  
Db 2146 ATAGATTTTGAAGGAGTTTATTTTATTTTATTTTATTTT 2182

RESULT 10

US-10-221-714A-27  
; Sequence 95, Application US/10221714A  
; Publication No. US20040048254A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with  
; FILE OF INVENTION: tumor suppressor genes and oncogenes  
; FILE REFERENCE: 5013.1005  
; CURRENT APPLICATION NUMBER: US/10/221,714A  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: PCT/EP01/02955  
; PRIOR FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: DE 10013847.0  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 540  
; SEQ ID NO 27  
; LENGTH: 8666  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-221-714A-27

Query Match 15.2%; Score 106.6; DB 8; Length 8666;  
Best Local Similarity 49.0%; Pred. No. 1.9e-09;  
Matches 312; Conservative 0; Mismatches 324; Indels 1; Gaps 1;

Qy 12 AAAGTTTTTTTTTTTGGATGATTTTAAATAAAATCATTTTCTTTTTTATTTATTTAT 71  
Db 1547 AAAGTTTTTTTATTTATTTTAAATTTATTTATATAATATTTTAAATTTTATTTATTTA 1606  
Qy 72 ACTTTTAAGTTTTRAGGTCATCATGTCAAAAGTGTGCAGGTTAGTTTACATATATATACATGT 131  
Db 1607 TATTTTAAAGTTTTRAGAGTATATGTATAATGTCGTAGGTTTGTATATATATATATATGT 1666  
Qy 132 GCCATGCTGCTGCTGCCACCCATTAACCTACATGCAAGTGTTTTTTAAATTTTAAATTTAGTGACA 191  
Db 1667 GTTATGTTGGTGTGTTGTTATTTATTAATTTA -TTATTTAGTATTAGGTATATTTTAAAT 1725  
Qy 192 GTTTTACTGATTTTCCCTAAATTTGAAAGTATCATAGTAATCCATAAAATTTGAAAAAATGT 251  
Db 1726 GTTATTTTATTTTATTTTATTTTATTAAGATTTTATAAGTATTTATAAGTAAATGGAATTTTAAATTTT 1785  
Qy 252 TAACCTACTCTGATAAAAAAGTTTATAGTTTCCCTACTTTTAAAGCAAAATTCATAGGGCA 311  
Db 1786 AGAGTAAATGGTTTATTTTAAAGGATGTTATAATTTTATTTTATTTTATTTTATTTTATTTT 1845  
Qy 312 TGGTAATGTAGTTTCAACATTACTTGCAGTTTCAGTTAGTAATAATAATTAAGCCCTAG 371  
Db 1846 GAGATATATATATAAAATTTGTTTGGTATTTTAAAGTAGTTAAATTTTATTTTATTTTATTTT 1905  
Qy 372 TAAGTATAATTTAATATTTGTCAAATAATTTGCAAAATACCATGGGTACTTTAAATTTGATTTT 431  
Db 1906 TTTATATAGTATTTAAATGTTGTTTTTATATGTTGTTATTTTATTTTATTTTATTTTATTAATA 1965  
Qy 432 ACCAAATTTCCATGGAACAACAAGTTGGCTATTTTGGATTGATATTTTGGATTGATATTTTGAATACT 491  
Db 1966 GTTATATATATTTTATAAGAGTTGAAAGAGTTTTCGATCTAGCAATTTATGTTAGT 2025  
Qy 492 AGTACAGGAATATCATTTGTTAGTTGAAATTTTAGCCTTAGAAAACAATGAGTTAGAT 551  
Db 2026 TTTAGAGAAATTTTGAATTTTATTTGAAAGTTTATTTTATTTTATTTTATTTTATTTT 2085  
Qy 552 AGCTAAAGTATAATTTATTTGCTGATTTAATAATGATGATGAGTTAGGGCTATGATAATTA 611  
Db 2086 TATTTTATTTTAAAAAATTAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 2145  
Qy 612 GTGAAAACACCCCAAGAATGTTTATACCTTTTAAATTT 648  
Db 2146 ATAGATTTTGAAGGAGTTTATTTTATTTTATTTTATTTTATTTTATTTT 2182

RESULT 11

US-10-311-507-95  
; Sequence 95, Application US/10311507  
; Publication No. US20040115630A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Method and nucleic acids for the analysis of astrocytomas  
; FILE REFERENCE: 5013.1013  
; CURRENT APPLICATION NUMBER: US/10/311,507  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: PCT/EP01/07538  
; PRIOR FILING DATE: 2001-07-02  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 136  
; SEQ ID NO 95  
; LENGTH: 8666  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-311-507-95

Query Match 15.2%; Score 106.6; DB 8; Length 8666;

Best Local Similarity 49.0%; Pred. No. 1.9e-09;		
Matches 312;	Conservative 0;	Mismatches 324; Indels 1; Gaps 1;
QY	12	AAAGTTTTTTTTTTTGATGATTTTAAATAAAATATCATTTTTCTTTTTTATTATTATTAT 71
DB	1547	AAAGTTTTTTTATATATATTTAAATTTATATAATATTTTTTAAATTTTATATTATTAA 1606
QY	72	ACTTTTAAAGTTTTAGGGTACATGTCAAAGTGTGCAGTTAGTTTACATATATATACATGT 131
DB	1607	TATTTTAAAGTTTTAGAGTATATGTGATAATGTGTAGGTTTGTATATATATGTATATATGT 1666
QY	132	GCCATGCTGTGTGCTGCCACCCATAACTCACATGAAGTTTTTTTTTAAATTTTAGTGACA 191
DB	1667	GTTATGTGTGTGTGTATTTTATTAATTTTA-TTATTTTAGTATTAGGTATATTTTTTTAAAT 1725
QY	192	GTTTTAGTCATTTTTCTTAAATGAAAGTATCATTAAGTAATCCATAAATTTGAAAAAAATGT 251
DB	1726	GTTATTTTTTTTTTTTTTTTTTATATAGATTTTATTAAGTATTAATCGATATCGATTTTAAITTTT 1785
QY	252	TAACTACTCTGATAAAAAAGTTTTTATAGTTTCCTACTTTTAAAGCAAAATTTCCATAGGCCA 311
DB	1786	AGAGTAAATGGTTTTTATTTTAAAGGATGTTATAAATTTTTTTTAGAGTTTATTTGTAAGATAT 1845
QY	312	TGTTAATTGTAGTTTCAACATTACTTGCAGTTTCAGTTAGTAATAAATATTAAAGCCTAG 371
DB	1846	GAGATATATATATTTAAAAATTTGTTTTGGTATTTTTTAAAGTAGTAAATTTTTTATATTTG 1905
QY	372	TAAGTATAATTTAAATATTGTGCAAAATAATTTGGAAAAATACCATGGGTACTTTAAATGATTTT 431
DB	1906	TTTTATAATGATTTTAAATGTGTTTTTATATGGTTGTATTTTTTATTTTTTTTATTAAATA 1965
QY	432	ACCAAAATTTCCATGGAAACAAACAGGTGGCTATTTTTTCGAATGTATATTTTGAATFAC 491
DB	1966	GTTTATATATTTTTTTATAAGAGTTGAAAGAGTTTTTTTGATGTAGGAATTTATGCTAGAGT 2025
QY	492	AGTACAGGAATATCATGTTTAGTTGAATTTTTTAGCCCTTAGAAAAACAATGGAGTTTAGAT 551
DB	2026	TTTTAGAGAAATTTTTTGAAATTTATTTGAAGTTTTTATTTTAGAAATATATGTGTAAAGTAATA 2085
QY	552	AGCTAAAGTATAATTTTATTTGTGATTTTAAATAGGTATGGAGTTAGGGCTATGATAATTA 611
DB	2086	TATTTTTTTTAAAAAAATTTATTTATTTTTTTTTTTTTTTTTCGAGAAGAGGTATTTATTTTA 2145
QY	612	GTGAAACACCCAGGAATGTTTTATACCTTTTAAATTT 648
DB	2146	ATAGATTTTTTGAAGGAGTTTATTTTTTTTTTTTATTTTTTTT 2182

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RESULT 12
US-10-433-793-207
; Sequence 207, Application US/10433793
; Publication No. US20040142334A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/433,793
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 212
; SEQ ID NO 207
; LENGTH: 8666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-433-793-207

```

```

RESULT 13
US-09-925-065A-477191/c
; Sequence 477191, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; NUCLEOTIDE POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 477191
; LENGTH: 493
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-477191
Query Match 15.1%; Score 105.8; DB 4; Length 493;

```





```
QY 72 ACTTTAAAGTTTGGGTACATGTGCAAGTGTGAGGTTAGTTACATATATACATGT 131
|||
Db 395 AC-TTTAAAGTTTGGGTACATGTGCAAGTGTGAGGTTAGTTACATATATACATGT 337
|||
QY 132 GCCATGCTGGTGTGTCGACCCATTAACTACATGAAAGTGTGTTTAAATTTAGTGACA 191
|||
Db 336 GCCATGCTGGTGTGTCGACCCATTAACTC---GTCAATTAGCAATTAGGTATATCTCCTA 280
|||
QY 192 GTTTTAGTCATTTTCTTAATGAAAGTATCAATGTAATCCATAAATTTGAAAAAATGT 251
|||
Db 279 ATGCTATCCCTCCCTTATTAATATATCTTATGTCATAAATATATTATTATAAAATGT 220
|||
QY 252 TAACTACTCTGATATAAAAGTTTATAGTTTCTTACTTTTA 292
|||
Db 219 TTTCTGTTTAAATGATATTATCAATGTTTAGTGTTTA 179
|||
RESULT 19
US-10-304-113-4
; Sequence 4, Application US/10304113
; Publication No. US20040102623A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF PAK1 EXPRESSION
; FILE REFERENCE: RTS-0415
; CURRENT APPLICATION NUMBER: US/10/304,113
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 167
; SEQ ID NO 4
; LENGTH: 70043
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-304-113-4
Query Match 15.1%; Score 105.6; DB 8; Length 70043;
Best Local Similarity 78.8%; Pred. No. 5.7e-09;
Matches 126; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 2 TGTTCACATAAAGTTTATTTTGGTGAATTTTAAATAATATCATTTCTTTTAA 61
|||
Db 60893 TATTTTATTTATTTTATTTTCTTTTCTTTTAAATCTTTTAAATTTTACATTTTA 60952
|||
QY 62 TTATTTATTTACTTTTAAAGTTTGGGTACATGTGCAAGTGTGAGGTTAGTTACATAT 121
|||
Db 60953 TTATTTATTTACTTTTAAAGTTTGGGTACATGTGCAAGTGTGAGGTTAGTTACATAT 61012
|||
QY 122 ATATACATGTGCCATGCTGCTGTCGCCATTAATCACTC 161
|||
Db 61013 GTATACATGTACCAATGTTGGTGTGCTGTACCAATTAATCACTC 61052
|||
RESULT 20
US-10-027-632-267264/c
; Sequence 267264, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267264
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
US-10-027-632-267265/c
; Sequence 267265, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267265
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
US-10-027-632-267265/c
```

```
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267264
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
US-10-027-632-267264
Query Match 15.1%; Score 105.4; DB 6; Length 563;
Best Local Similarity 65.5%; Pred. No. 1.3e-09;
Matches 184; Conservative 1; Mismatches 92; Indels 4; Gaps 2;
QY 12 AAAGTTTTTTTTTGTGATGATTTTAAATAAATATCATTTTCTTTTATTATTATTAT 71
|||
Db 455 AATATTATATACATATTTAAATGATATTATTATTCAATATCTTTTWTATTATTAT 396
|||
QY 72 ACTTTAAAGTTTGGGTACATGTGCAAGTGTGAGGTTAGTTACATATATACATGT 131
|||
Db 395 AC-TTTAAAGTTTGGGTACATGTGCAAGTGTGAGGTTAGTTACATATATACATGT 337
|||
QY 132 GCCATGCTGGTGTGTCGCCATTAATCAATGTAATCCATAAATTTTAAATTTAGTGACA 191
|||
Db 336 GCCATGCTGGTGTGTCGCCATTAATCAATGTAATCCATTAATCTCCTTATCTCCTA 280
|||
QY 192 GTTTTAGTCATTTTCTTAATGAAAGTATCATAGTAATCCATAAATTTGAAAAAATGT 251
|||
Db 279 ATGCTATCCCTCCCTTATTAATATATCTTATGTCATAAATATATTATTATAAAATGT 220
|||
QY 252 TAACTACTCTGATATAAAAGTTTATAGTTTCTTACTTTTA 292
|||
Db 219 TTTCTGTTTAAATGATATTATTCAATGTTTAGTGTTTA 179
|||
RESULT 21
US-10-027-632-267265/c
; Sequence 267265, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267265
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
US-10-027-632-267265
Query Match 15.1%; Score 105.4; DB 6; Length 563;
```



	Query Match	Best Local Similarity	15.1%	Score 105.4	DB 6	Length 600
	Matches 148	Conservative	2	Mismatches 48	Indels 5	Gaps 1
QY	3	GTTCACATAAAGTTTTTTTTTTTGTAGATTTTAATAAATAATCAATTTCTTTTTTAT	62			
Db	402	GTTGAAGAGACATTTCTTTTTTTTTTTTTCATTTTAAAGCATTTTAAATTTCTTTTTTAAAA	343			
QY	63	TATATTATACT-----TTTAAAGTTTTAGGTCATGTGCAAAAGTCGACAGGTAGTTAC	117			
Db	342	TTTTTATATATATACATTTTAAAGTTTTTAGGTCATGTGCACATGTGACAGGTAGTTAC	283			

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QY 118 ATATATATACATGCGCATCTGGTGTGCGACCCCACTTAACATCAATGAGTTTTCAT 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 ATATGTATACATGTGYCATCTGATGTGCTGCACCCCACTTAACATCAATGAGTTAT 223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 178 AAATTTTGTAGTGACAGTTTTCATGTC 200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 222 ATCTCCTAATGCTATCCCTACYC 200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

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RESULT 27
US-10-027-632-235941/c
; Sequence 235941, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235941
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235941
```

```
Query Match 15.1%; Score 105.4; DB 7; Length 600;
Best Local Similarity 72.9%; Pred. No. 1.3e-09;
Matches 148; Conservative 2; Mismatches 48; Indels 5; Gaps 1;
```

```
QY 3 GTTTCACATAAAGTTTTTTTTTTTGGATGATTTTAAATAAAATATCAATTTCTTTTAT 62
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 GTTGAAGAGACATTTCTTTTTTTTTCATTTTAAGCATTTTAAATTTCTTTTAAAA 343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 63 TATTATTACT-----TTTAAGTTTGGGTACATGCGCAAGTGTGCGAGTTAGTTAC 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 TTTTATTATTATATCTTTAAAGTTTGGGTACATGTCACCAATGTCAGGTTAGTTAC 283
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 118 ATATATATACATGCGCATCTGGTGTGCGACCCCACTTAACATCAATGAGTTTTCAT 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 ATATGTATACATGTGYCATCTGATGTGCTGCACCCCACTTAACATCAATGAGTTAT 223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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```
QY 178 AAATTTTGTAGTGACAGTTTTCATGTC 200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 222 ATCTCCTAATGCTATCCCTACYC 200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 28
US-10-027-632-235942/c
; Sequence 235942, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
```

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; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235942
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235942
```

```
Query Match 15.1%; Score 105.4; DB 7; Length 600;
Best Local Similarity 72.9%; Pred. No. 1.3e-09;
Matches 148; Conservative 2; Mismatches 48; Indels 5; Gaps 1;
```

```
QY 3 GTTTCACATAAAGTTTTTTTTTTTGGATGATTTTAAATAAAATATCAATTTCTTTTAT 62
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 GTTGAAGAGACATTTCTTTTTTTTTCATTTTAAGCATTTTAAATTTCTTTTAAAA 343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 63 TATTATTACT-----TTTAAGTTTGGGTACATGTCGCAAGTGTGCGAGTTAGTTAC 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 TTTTATTATTATATCTTTAAAGTTTGGGTACATGTCACCAATGTCAGGTTAGTTAC 283
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 118 ATATATATACATGCGCATCTGGTGTGCTGCACCCCACTTAACATCAATGAGTTTTCAT 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 ATATGTATACATGTGYCATCTGATGTGCTGCACCCCACTTAACATCAATGAGTTAT 223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
QY 178 AAATTTTGTAGTGACAGTTTTCATGTC 200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 222 ATCTCCTAATGCTATCCCTACYC 200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 29
US-10-027-632-235943/c
; Sequence 235943, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235943
```



```
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235943

Query Match      15.1%; Score 105.4; DB 7; Length 600;
Best Local Similarity 72.3%; Pred. No. 1.3e-09;
Matches 148; Conservative 2; Mismatches 48; Indels 5; Gaps 1;

QY 3 GTTTCACATAAGTTTTTTTTTTTGGATGATTTTAAATAAATATCATTTCTTTTAT 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 GTTGAAGACATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 343
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 63 TATTATTATAC-----TTTAAAGTTTGGGTACATGTGCAAGTGTGCAGTTAGTTAC 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 TTTTATTATTATACTTTAAAGTTTGGGTACATGTGCACATGTGCAGTTAGTTAC 283
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 118 ATATATATACATGTGCCATGTGCTGTCGCCATTAACATCAATCAATGTTT 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 ATATGTATACATGTGTCATGTGCTGCCATTAACATCAATGTTT 223
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 178 AAATTTTAGTGACATTTTATGTC 200
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 222 ATCTCTAATGCTATCCCTACYC 200
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 30
US-09-818-657-3/C
; Sequence 3, Application US/09818657
; Publication No. US2003007773A1
; GENERAL INFORMATION:
; APPLICANT: BRANDON, Rhonda et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001006-CIP
; CURRENT APPLICATION NUMBER: US/09/818,657
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 2001-03-28
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Human
US-09-818-657-3

Query Match      15.1%; Score 105.4; DB 3; Length 82938;
Best Local Similarity 82.3%; Pred. No. 6.6e-09;
Matches 121; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGGATGATTTTAAATAAATATCATTTCTTTTATTTATTTATTTACTT 75
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63261 TCCTTGGTTTATGTGGAACAATTTGTTTATTTTATTTATTTATTTATTTACTT 63202
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 76 TTAAGTTTGGGTACATGTGCAAGTGTGCAGTTAGTTACATATATATACATGTGCCA 135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63201 TTCAGTTTGGGTACATGTGCAATGTGCAGTTAGTTACATATATATACATGTGCCA 63142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 31
US-11-136-623-3/c
; Sequence 3, Application US/11136623
; Publication No. US20050221437A1
; GENERAL INFORMATION:
; APPLICANT: BRANDON, Rhonda, et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
```

```
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001006-CIPCON
; CURRENT APPLICATION NUMBER: US/11/136,623
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: 09/730,002
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 82938
; TYPE: DNA
; ORGANISM: Human
US-11-136-623-3

Query Match      15.1%; Score 105.4; DB 13; Length 82938;
Best Local Similarity 82.3%; Pred. No. 6.6e-09;
Matches 121; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGGATGATTTTAAATAAATATCATTTCTTTTATTTATTTATTTACTT 75
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63261 TCCTTGGTTTATGTGGAACAATTTGTTTATTTTATTTATTTATTTATTTACTT 63202
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 76 TTAAGTTTGGGTACATGTGCAAGTGTGCAGTTAGTTACATATATATACATGTGCCA 135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63201 TTCAGTTTGGGTACATGTGCAATGTGCAGTTAGTTACATATATATACATGTGCCA 63142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 136 TGCTGGTGTGCTGCCACCACTTAACCTCA 162
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63141 TGCTGGTGTGCTGCCACCACTTAACCTCA 63115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 32
US-10-301-480-578850
; Sequence 578850, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 578850
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155,
; LOCATION: 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167,
; LOCATION: 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179,
; LOCATION: 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202,
; LOCATION: 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214,
; LOCATION: 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226,
; LOCATION: 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 238, 239, 240, 241, 242, 243
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-578850

Query Match      15.0%; Score 105.2; DB 12; Length 989;
```

```
Best Local Similarity 79.1%; Pred. No. 1.7e-09;
Matches 125; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4 TTTACATAAAGTTTTTTTTTTTGGATGATTTTAATAAAATATATCTTTCTTTTATT 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 441 TGTCCAAAGCATTAATTTATTTATTTTATTTTGGCGTAATTTATTTATTTATT 500

QY 64 ATTATTATACATTTTAAGTTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATAT 123
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 501 ATTACAGTACTTTTAAGTTTTTAGGTACATGTGCACAATGTGCAGGTAGTTACATAT 560

QY 124 ATACATGTGCATGCTGCTGCTGTGCACCATTAACTC 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 561 ATACATGTGCATGCTGCTGCTGCTGCACCATTAACTC 598

RESULT 33
US-10-301-480-1192259
; Sequence 1192259, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1192259
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155,
; LOCATION: 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167,
; LOCATION: 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179,
; LOCATION: 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202,
; LOCATION: 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214,
; LOCATION: 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226,
; LOCATION: 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 238, 239, 240, 241, 242, 243
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-1192259

Query Match 15.0%; Score 105.2; DB 12; Length 989;
Best Local Similarity 79.1%; Pred. No. 1.7e-09;
Matches 125; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4 TTTACATAAAGTTTTTTTTTTTGGATGATTTTAATAAAATATATCTTTCTTTTATT 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 441 TGTCCAAAGCATTAATTTATTTATTTTATTTTGGCGTAATTTATTTATTTATT 500

QY 64 ATTATTATACATTTTAAGTTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATAT 123
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 501 ATTACAGTACTTTTAAGTTTTTAGGTACATGTGCACAATGTGCAGGTAGTTACATAT 560

QY 124 ATACATGTGCATGCTGCTGCTGTGCACCATTAACTC 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 561 ATACATGTGCATGCTGCTGCTGCTGCACCATTAACTC 598
```

```
RESULT 34
US-11-121-086-51
; Sequence 51, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 51
; LENGTH: 176760
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-51

Query Match 15.0%; Score 104.8; DB 15; Length 176760;
Best Local Similarity 87.5%; Pred. No. 1.1e-08;
Matches 126; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 17 TTTTGTGATGATTTTAAATAAAATATCATTTTCTTTTATTTATTTATTTT 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20705 TTTTATTTTAAATTTTATTTTAAATTTCTTTTATTTATTTATTTATTT 20763

QY 77 TAAATTTTAGGGTACATGTGCAAAAGTGTGCAGGTAGTTACATATATACATGTGCCAT 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20764 TAAATTTTAGGGTACATGTGCATAATGTGCAGGTAGTTACATATATACATGTGCCAT 20823

QY 137 GCTGGTGTGCTGCCACCATTAAC 160
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20824 GCTGGTGTGCTGCCACCATTAAC 20847

RESULT 35
US-10-322-281-214
; Sequence 214, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandino
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 72678
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-281-214

Query Match 14.9%; Score 104.6; DB 8; Length 72678;
Best Local Similarity 80.8%; Pred. No. 8.9e-09;
Matches 122; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 11 TAAAGTTTTTTTTTTTGGATGATTTTAAATAAAATATCATTTTCTTTTATTTATTTA 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68541 TACAGAACTCTTTTTTTTTTTTCTCTCTCTATATATTTTATTTATTTATTTA 68600

QY 71 TACTTTTAAAGTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATACATG 130
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68601 TACTTTTAAAGTTTTAGGTACATGTGCACAATGTGCAGGTAGTTACATATGATACATG 68660

QY 131 TGCCATGCTGGTGTGCTGCCACCATTAAC 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68661 TGCCATGCTGGTGTGCTGCCACCATTAAC 68691
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[illegible]



Db 39078 ACATGTGCCATGCTGCTGTGCTGCACCCATTAACTC 39113

## RESULT 43

US-10-517-905-19/c  
; Sequence 19, Application US/10517905  
; Publication No. US20060084142A1  
; GENERAL INFORMATION:  
; APPLICANT: Oregon Health & Science University  
; APPLICANT: Michael, Heinrich Charles  
; APPLICANT: Corless, Christopher Lee  
; APPLICANT: Fletcher, Jonathan Alfred  
; APPLICANT: Demetri, George D.  
; TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR  
; FILE REFERENCE: 899-65892-02  
; CURRENT APPLICATION NUMBER: US/10/517,905  
; CURRENT FILING DATE: 2004-12-10  
; PRIOR FILING DATE: 2002-06-13  
; PRIOR FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: US 60/438,899  
; PRIOR FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 191150  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (1)..(49)  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: (50)..(2330)  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (2331)..(2648)  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: (2649)..(4902)  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (4903)..(5163)  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: (5164)..(6154)  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (6155)..(6285)  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: (6286)..(8524)  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (8525)..(8696)  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: (8697)..(8787)  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (8788)..(8977)  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: (8978)..(166510)  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: (10577)..(10676)  
; OTHER INFORMATION: n = any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (10577)..(10676)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: (14335)..(14434)  
; OTHER INFORMATION: n = any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (14335)..(14434)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: (16247)..(16346)  
; OTHER INFORMATION: n = any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (16247)..(16346)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (17457)..(17457)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (21818)..(21818)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (36293)..(36298)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (36314)..(36314)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (36316)..(36316)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (36432)..(36433)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: (36774)..(36873)  
; OTHER INFORMATION: n = any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (36774)..(36873)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: (59740)..(59740)  
; OTHER INFORMATION: n = any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (59740)..(59740)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: (59742)..(59742)  
; OTHER INFORMATION: n = any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (59742)..(59744)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: (59744)..(59744)  
; OTHER INFORMATION: n = any nucleic acid  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: (59749)..(59755)  
; OTHER INFORMATION: n = any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature

```
; LOCATION: (59749)..(59755)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (59759)..(59760)
; OTHER INFORMATION: n = any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (59759)..(59760)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (59765)..(59766)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (59776)..(59875)
; OTHER INFORMATION: n = any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (59776)..(59875)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (82745)..(82844)
; OTHER INFORMATION: n = any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (82745)..(82844)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (96508)..(96607)
; OTHER INFORMATION: n = any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (96508)..(96607)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (147675)..(147774)
; OTHER INFORMATION: n = any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (147675)..(147774)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (157152)..(157251)
; OTHER INFORMATION: n = any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (157152)..(157251)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (161475)..(161574)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
```

```
Query Match 14.9%; Score 104; DB 12; Length 191150;
Best Local Similarity 83.3%; Pred. No. 1.6e-08;
Matches 130; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

QY 6 TCACATAAAGTTTTTTTTTTTGGATGATTTTAATAAAATATCATTTTCTTTTTTTTATAT 65
Db 35430 TCTATTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 35371

QY 66 TATTATATCTTTTAAGTTTTTAGGGTACATGTGCAAGTGTCAGGTAGTTACATATATAT 125
Db 35370 TATTATATAC-TTTTAAGTTTTTAGGGTACATGTGCAATGTCAGGTAGTTACATATGAT 35312

QY 126 ACATGTGCCATGCTGGTGTGTCGCCACCACTTAACTC 161
```

```
Db 35311 ACATGTGCCATGCTGGTGTGTCGCCACCACTTAACTC 35276

RESULT 44
US-10-087-192-1330/c
; Sequence 1330, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1330
; LENGTH: 102980
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-1330
```

```
Query Match 14.8%; Score 103.8; DB 6; Length 102980;
Best Local Similarity 81.6%; Pred. No. 1.4e-08;
Matches 120; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 15 GTTTTTTTTTTTGGATGATTTTAATAAAATATCATTTTCTTTTTTTTATTTATTTACT 74
Db 84334 GCTTTTTTATTTATTTATTTTATTTTATTTATATATATATATTTTCTTTTTTACT 84275

QY 75 TTTAAGTTTTTAGGTACATGTGCAAGTGTCAGGTAGTTACATATATATACATGTGCC 134
Db 84274 TTTAAGTTTTTAGGTACATGTGCACATTTGGCAGGTAGTTACATATGTACATGTGCC 84215

QY 135 ATGCTGGTGTGTCGCCACCACTTAACTC 161
Db 84214 ATGCTGGTGTGTCGCCACCACTTAACTC 84188
```

```
RESULT 45
US-10-741-600-17645
; Sequence 17645, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17645
; LENGTH: 103660
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)....(103660)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-7)
US-10-741-600-17645
```

```
Query Match 14.8%; Score 103.8; DB 9; Length 103660;
Best Local Similarity 87.4%; Pred. No. 1.4e-08;
Matches 125; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 19 TTTTTTTTGGATGATTTTAATAAAATATCATTTTCTTTTTTTTATTTATTTATTTACTTTTA 78
```

Db	52806	TTTTTTTTTTTTTTTGGAAATGGAGTTTCAGTCTCTTTTTTATTATTATAC-TTTA	52864
Qy	79	AGTTTTAGGGTACATGTGCACAAGTGTCAGGTTAGTTACATATATATACATGTGCCATGC	138
Db	52865	AGTTTTAGGGTACATGTGCACAATGTGCAGGTTAGTTACATATGTATACATGTGCCATGC	52924
Qy	139	TGGTGTGCTGCACCATAACTC	161
Db	52925	TGGTGTACCGCACCAITTAATC	52947
<b>RESULT 46</b>			
US-10-995-561-13253			
; Sequence 13253, Application US/10995561			
; Publication No. US20050272054A1			
; GENERAL INFORMATION:			
; APPLICANT: CARGILL, Michele et al.			
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH			
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF			
; TITLE OF INVENTION: DETECTION AND USES THEREOF			
; FILE REFERENCE: CL001559			
; CURRENT APPLICATION NUMBER: US/10/995,561			
; CURRENT FILING DATE: 2004-11-24			
; NUMBER OF SEQ ID NOS: 85702			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 13253			
; LENGTH: 103660			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (1)...(103660)			
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1			
US-10-995-561-13253			
Query Match 14.8%; Score 103.8; DB 10; Length 103660;			
Best Local Similarity 87.4%; Pred. No. 1.4e-08;			
Matches 125; Conservative 0; Mismatches 17; Indels 1; Gaps 1;			
Qy	19	TTTTTTTTTTCATGATTTTAAATAAATCATTTTCTTTTATTTATTTATATATATATTTTA	78
Db	52806	TTTTTTTTTTTTTTTGGAAATGGAGTTTCAGTCTCTTTTTTATTATTATAC-TTTA	52864
Qy	79	AGTTTTAGGGTACATGTGCACAAGTGTCAGGTTAGTTACATATATATACATGTGCCATGC	138
Db	52865	AGTTTTAGGGTACATGTGCACAATGTGCAGGTTAGTTACATATGTATACATGTGCCATGC	52924
Qy	139	TGGTGTGCTGCACCATAACTC	161
Db	52925	TGGTGTACCGCACCAITTAATC	52947
<b>RESULT 47</b>			
US-10-301-480-577167			
; Sequence 577167, Application US/10301480			
; Publication No. US20060057564A1			
; GENERAL INFORMATION:			
; APPLICANT: Wang, David G.			
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms			
; TITLE OF INVENTION: In the Human Genome			
; FILE REFERENCE: 108827.137			
; CURRENT APPLICATION NUMBER: US/10/301,480			
; CURRENT FILING DATE: 2002-11-21			
; PRIOR APPLICATION NUMBER: US 10/215,598			
; PRIOR FILING DATE: 2002-08-09			
; PRIOR APPLICATION NUMBER: US 60/311,695			
; PRIOR FILING DATE: 2001-08-10			
; NUMBER OF SEQ ID NOS: 1226818			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 577167			
; LENGTH: 987			
; TYPE: DNA			





Sequence 661, Application US/10074095  
Publication No. US20030077704A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC008C1  
CURRENT APPLICATION NUMBER: US/10/074,095  
CURRENT FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: 09/764,860  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/214,886  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 60/217,487  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,758  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/220,963  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/217,496  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: 60/225,447  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/218,290  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 60/225,757  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/226,868  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/216,647  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/225,267  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/216,880  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/225,270  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/251,869  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/235,834  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/234,274  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: 60/234,223  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: 60/228,924  
PRIOR FILING DATE: 2000-08-30  
PRIOR APPLICATION NUMBER: 60/224,518  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,369  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/224,519  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/220,964  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/241,809  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/249,299  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/236,327  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/241,785  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/244,617  
PRIOR FILING DATE: 2000-11-01  
PRIOR APPLICATION NUMBER: 60/225,268  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/236,368  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/251,856  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/251,868  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/229,344  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/234,997  
PRIOR FILING DATE: 2000-09-25  
PRIOR APPLICATION NUMBER: 60/229,343  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,345  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,287  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/229,513  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/231,413  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/229,509  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: 60/236,367  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/237,039  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,038  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/236,370  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/236,802  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,037  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/237,040  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 60/240,960  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/239,935  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/239,937  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/241,787  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/246,474  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/246,532  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/249,216  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,210  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/226,681  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,759  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/225,213  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/227,182  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/225,214  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/235,836  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/230,438  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/215,135  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 60/225,266  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: 60/249,218  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,208  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,213  
PRIOR FILING DATE: 2000-11-17

; PRIOR APPLICATION NUMBER: 60/249,212  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,207  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,245  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,244  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,217  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,211  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,215  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,264  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,214  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,297  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/232,400  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/231,242  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/232,081  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/232,080  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,414  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,244  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,064  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/233,063  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,397  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,399  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,401  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/241,808  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,826  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,786  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,221  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,475  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/231,243  
; PRIOR FILING DATE: 2000-09-08

Query Match 14.7%; Score 103.2; DB 6; Length 24132;  
Best Local Similarity 83.6%; Pred. No. 1.1e-08;  
Matches 117; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
  
QY 21 TTTTGTGATGATTTTAAATAAATATCATTTTCTTTTATTTATTTATTTATTTTAAAG 80  
Db 19204 TTTATTTTAAATTTTAAACATTTTCTTTTATTTTATTTTATTTTAAAG 19145  
  
QY 81 TTTTAGGGTACATGCGAAGTGTGCAGGTTAGTTACATATATATACATGTGCCATGCTG 140  
Db 19144 TTTTAGGGTACATGCGAAGTGTGCAGTTAGTTACATATGTATACATGTGCATGCTG 19085  
  
QY 141 GTGTGCTGCACCCCACTTA 160  
Db 19084 GTGCGCTGCACCCCACTTA 19065

RESULT 53

US-10-212-872-661/c  
; Sequence 661, Application US/10212872  
; Publication No. US20030215893A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC008C2  
; CURRENT APPLICATION NUMBER: US/10/212,872  
; CURRENT FILING DATE: 2002-08-07  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 1198  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 661  
; LENGTH: 24132  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-212-872-661  
  
Query Match 14.7%; Score 103.2; DB 7; Length 24132;  
Best Local Similarity 83.6%; Pred. No. 1.1e-08;  
Matches 117; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
  
QY 21 TTTTGTGATGATTTTAAATAAATATCATTTTCTTTTATTTATTTATTTTAAAG 80  
Db 19204 TTTATTTTAAATTTTAAACATTTTCTTTTATTTTATTTTATTTTAAAG 19145  
  
QY 81 TTTTAGGGTACATGCGAAGTGTGCAGGTTAGTTACATATATATACATGTGCCATGCTG 140  
Db 19144 TTTTAGGGTACATGCGAAGTGTGCAGTTAGTTACATATGTATACATGTGCATGCTG 19085  
  
QY 141 GTGTGCTGCACCCCACTTA 160  
Db 19084 GTGCGCTGCACCCCACTTA 19065

RESULT 54  
US-10-330-773-76/c  
; Sequence 76, Application US/10330773  
; Publication No. US20060040262A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001300  
; CURRENT APPLICATION NUMBER: US/10/330,773  
; CURRENT FILING DATE: 2002-12-27  
; NUMBER OF SEQ ID NOS: 991  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 76  
; LENGTH: 118544  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-330-773-76  
  
Query Match 14.7%; Score 103.2; DB 11; Length 118544;  
Best Local Similarity 83.6%; Pred. No. 1.9e-08;  
Matches 117; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
  
QY 21 TTTTGTGATGATTTTAAATAAATATCATTTTCTTTTATTTATTTATTTTAAAG 80  
Db 113985 TTTATTTTAAATTTTAAACATTTTCTTTTATTTTATTTTATTTTAAAG 113926  
  
QY 81 TTTTAGGGTACATGCGAAGTGTGCAGGTTAGTTACATATATATACATGTGCCATGCTG 140  
Db 113925 TTTTAGGGTACATGCGAAGTGTGCAGTTAGTTACATATGTATACATGTGCATGCTG 113866  
  
QY 141 GTGTGCTGCACCCCACTTA 160  
Db 113865 GTGCGCTGCACCCCACTTA 113846

RESULT 55  
US-10-301-480-570607

; Sequence 570607, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 570607  
; LENGTH: 865  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-570607

Query Match 14.7%; Score 103; DB 12; Length 865;  
Best Local Similarity 85.7%; Pred. No. 4.1e-09;  
Matches 126; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

QY 15 GTTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTATTATTACT 74

Db 653 GTTTTGTGATGATTTTAAATTTTAAATTTTATTATTATTATTATAC- 711

QY 75 TTTAAGTTTGGGTACATGTCGCAAGTGTGAGTTAGTTACATATATACATGTC 134

Db 712 TTTAAGTTTGGGTACATGTCGCAATGTGAGTTAGTTACATACGTATACATTTGCC 771

QY 135 ATGCTGGTGTGCTGCACCCATAACTC 161  
Db 772 ATGCTGGTGTGCTGCACCCATAACTC 798

## RESULT 56

US-10-301-480-1184016  
; Sequence 1184016, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1184016  
; LENGTH: 865  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-1184016

Query Match 14.7%; Score 103; DB 12; Length 865;  
Best Local Similarity 85.7%; Pred. No. 4.1e-09;  
Matches 126; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

QY 15 GTTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTATTATTACT 74

Db 653 GTTTTGTGATGATTTTAAATTTTAAATTTTATTATTATTATTATAC- 711

QY 75 TTTAAGTTTGGGTACATGTCGCAAGTGTGAGTTAGTTACATATATACATGTC 134

Db 712 TTTAAGTTTGGGTACATGTCGCAATGTGAGTTAGTTACATACGTATACATTTGCC 771

QY 135 ATGCTGGTGTGCTGCACCCATAACTC 161  
Db 772 ATGCTGGTGTGCTGCACCCATAACTC 798

## RESULT 57

US-10-301-480-552761/c  
; Sequence 552761, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 552761  
; LENGTH: 987  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-552761

Query Match 14.7%; Score 103; DB 12; Length 987;  
Best Local Similarity 82.5%; Pred. No. 4.2e-09;  
Matches 118; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 20 TTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTATTATTACTTTTAA 79

Db 493 TTTTGTGATGATTTTGTGTTATTATTATTATTATTATTATTATTATTATTAA 434

QY 80 GTTTTAGGTACATGTCGCAAGTGTGAGTTAGTTACATATATACATGTGCCATGCT 139

Db 433 GTTTTAGGTACATGTCGCAATGTGAGTTAGTTACATATATACATGTGCCATGCT 374

QY 140 GGTGTGCTGCACCCATAACTCA 162  
Db 373 GGTGTGCTGCACCCATAACTCA 351

## RESULT 58

US-10-301-480-1166170/c  
; Sequence 1166170, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1166170  
; LENGTH: 987  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-1166170

Query Match 14.7%; Score 103; DB 12; Length 987;  
Best Local Similarity 82.5%; Pred. No. 4.2e-09;  
Matches 118; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 20 TTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTATTATTACTTTTAA 79



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; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91798
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-91798

Query Match      14.7%; Score 102.8; DB 12; Length 729;
Best Local Similarity 81.5%; Pred. No. 4.2e-09;
Matches 119; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGGATGATTTTAATAAAATATCACTTTCTTTTATTATTATTACTT 75
Db 260 TTTACCTTTTCTTTCTTTTATTATTATTATTATTATTATTATTATTACTT 201

QY 76 TTAAGTTTTAGGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 135
Db 200 TTAAGTTTTAGGGTACATGTGCACACGTGCAGGTTTGTACATATGTATACATGTGCCA 141

QY 136 TGCTGGTGTGCTGCCACCACTTAACCTC 161
Db 140 TGTGGTGTGCTGCCACCACTTAACCTC 115

RESULT 64
US-10-301-480-91799/c
; Sequence 91799, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91799
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-91799

Query Match      14.7%; Score 102.8; DB 12; Length 729;
Best Local Similarity 81.5%; Pred. No. 4.2e-09;
Matches 119; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGGATGATTTTAATAAAATATCACTTTCTTTTATTATTATTACTT 75
Db 260 TTTACCTTTTCTTTCTTTTATTATTATTATTATTATTATTATTATTACTT 201

QY 76 TTAAGTTTTAGGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 135
Db 200 TTAAGTTTTAGGGTACATGTGCACACGTGCAGGTTTGTACATATGTATACATGTGCCA 141

QY 136 TGCTGGTGTGCTGCCACCACTTAACCTC 161
Db 140 TGTGGTGTGCTGCCACCACTTAACCTC 115

RESULT 63
US-10-301-480-91798/c
; Sequence 91798, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
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; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91798
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-91798

Query Match      14.7%; Score 102.8; DB 12; Length 729;
Best Local Similarity 81.5%; Pred. No. 4.2e-09;
Matches 119; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGGATGATTTTAATAAAATATCACTTTCTTTTATTATTATTACTT 75
Db 260 TTTACCTTTTCTTTCTTTTATTATTATTATTATTATTATTATTATTACTT 201

QY 76 TTAAGTTTTAGGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 135
Db 200 TTAAGTTTTAGGGTACATGTGCACACGTGCAGGTTTGTACATATGTATACATGTGCCA 141

QY 136 TGCTGGTGTGCTGCCACCACTTAACCTC 161
Db 140 TGTGGTGTGCTGCCACCACTTAACCTC 115

RESULT 62
US-10-027-632-256998/c
; Sequence 256998, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256998
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-256998

Query Match      14.7%; Score 102.8; DB 7; Length 729;
Best Local Similarity 81.5%; Pred. No. 4.2e-09;
Matches 119; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGGATGATTTTAATAAAATATCACTTTCTTTTATTATTATTACTT 75
Db 260 TTTACCTTTTCTTTCTTTTATTATTATTATTATTATTATTATTATTACTT 201

QY 76 TTAAGTTTTAGGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 135
Db 200 TTAAGTTTTAGGGTACATGTGCACACGTGCAGGTTTGTACATATGTATACATGTGCCA 141

QY 136 TGCTGGTGTGCTGCCACCACTTAACCTC 161
Db 140 TGTGGTGTGCTGCCACCACTTAACCTC 115

RESULT 63
US-10-301-480-91798/c
; Sequence 91798, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
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RESULT 65
US-10-301-480-705207/c
; Sequence 705207, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 705207
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-705207

Query Match      14.7%; Score 102.8; DB 12; Length 729;
Best Local Similarity 81.5%; Pred. No. 4.2e-09;
Matches 119; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY    16   TTTTTCCTTTTTTGATGATTTTAATAAAATACATATTTCTTTTTTATTATTATTATATCTT 75
DB    260  TTTCACCTTTTTTCTTTCTTTTTTAATTTTATTTTATTTTATTTTATTTTATTTATATCTT 201

QY    76   TTAAGTTTTTAGGTACATGTGC AAAGTGGCAGGTAGTTACATATATACATGTGCCA 135
DB    200  TTAAGTTTTTAGGTACATGTGC AACGTGCAGGTTGTACATATGTATACATGTGCCA 141

QY    136  TGCTGTGTGCTGCACCCCATTAATCT 161
DB    140  TGTGTGTGTGCTGCACCCCATTAATCT 115


RESULT 66
US-10-301-480-705208/c
; Sequence 705208, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 705208
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-705208

Query Match      14.7%; Score 102.8; DB 12; Length 729;
Best Local Similarity 81.5%; Pred. No. 4.2e-09;
Matches 119; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY    16   TTTTTCCTTTTTTGATGATTTTAATAAAATACATATTTCTTTTTTATTATTATTATCTT 75
DB    260  TTTCACCTTTTTTCTTTCTTTTTTAATTTTATTTTATTTTATTTTATTTTATATCTT 201

QY    76   TTAAGTTTTTAGGTACATGTGC AAAGTGGCAGGTAGTTACATATATACATGTGCCA 135
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Qy 137 GCTGGTGTGCTGCACCCCAATTAATC 161  
Db 9384 GCTGGTGTGCTGCACCCCAATTAATC 9360

## RESULT 69

US-09-984-429-448/c  
; Sequence 448, Application US/09984429  
; Publication No. US20040010132A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 53 Human Secreted Proteins  
; FILE REFERENCE: PZ018P2  
; CURRENT APPLICATION NUMBER: US/09/984,429  
; CURRENT FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: 60/244,591  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 09/288,143  
; PRIOR FILING DATE: 1999-04-08  
; PRIOR APPLICATION NUMBER: PCT/US98/21142  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/061,463  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/061,529  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/071,498  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/061,527  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/061,536  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/061,532  
; PRIOR FILING DATE: 1997-10-09  
; NUMBER OF SEQ ID NOS: 727  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 448  
; LENGTH: 26225.  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-984-429-448

Query Match 14.7%; Score 102.6; DB 3; Length 26225;  
Best Local Similarity 86.2%; Pred. No. 1.5e-08;  
Matches 125; Conservative 0; Mismatches 19; Indels 1; Gaps 1;  
Qy 17 TTTTCTTTTTCATGATTTTAAATAAATATCATTTCTTTTCTTTTATTTATTTATTTATTTT 76  
Db 9503 TTTTCTTTTTCATGATTTTAAATAAATATCATTTCTTTTCTTTTATTTATTTATTTATTT 9445  
Qy 77 TAAGTTTTCAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATATATATATATATAT 136  
Db 9444 TAAGTTTTCAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATATATATATATAT 9385  
Qy 137 GCTGGTGTGCTGCACCCCAATTAATC 161  
Db 9384 GCTGGTGTGCTGCACCCCAATTAATC 9360

## RESULT 70

US-10-091-504-1276/c  
; Sequence 1276, Application US/10091504  
; Publication No. US20030059908A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC007C1  
; CURRENT APPLICATION NUMBER: US/10/091,504  
; CURRENT FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 2442  
; Prior Application removed - See File Wrapper or Palm  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1276

; LENGTH: 26225  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-091-504-1276  
Query Match 14.7%; Score 102.6; DB 6; Length 26225;  
Best Local Similarity 86.2%; Pred. No. 1.5e-08;  
Matches 125; Conservative 0; Mismatches 19; Indels 1; Gaps 1;  
Qy 17 TTTTCTTTTTCATGATTTTAAATAAATATCATTTCTTTTCTTTTATTTATTTATTTATTTT 76  
Db 9503 TTTTCTTTTTCATGATTTTAAATAAATATCATTTCTTTTCTTTTATTTATTTATTTATTT 9445  
Qy 77 TAAGTTTTCAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATATATATATATATAT 136  
Db 9444 TAAGTTTTCAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATATATATATATAT 9385  
Qy 137 GCTGGTGTGCTGCACCCCAATTAATC 161  
Db 9384 GCTGGTGTGCTGCACCCCAATTAATC 9360

Search completed: July 19, 2006, 07:47:37  
Job time : 1473 secs

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OM nucleic - nucleic search, using sw model

Run on: July 19, 2006, 07:08:55 ; Search time 286 Seconds  
(without alignments)  
3516.007 Million cell updates/sec

Title: US-10-661-966-1\_146001-146700\_A146311  
Perfect score: 700  
Sequence: 1 ctgtttcacataaagtgtttt.....gccttttagtgatggtgga 700

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 899801 seqs, 718270062 residues  
Total number of hits satisfying chosen parameters: 1799602

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Listing first 70 summaries

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3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
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7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
9: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	110.8	15.8	1000	8	US-11-266-748A-196825
C 2	106.6	15.2	8666	6	US-10-517-441-283
C 3	106.6	15.2	8666	6	US-10-517-441-557
C 4	104.6	14.9	72678	6	US-10-539-228-214
C 5	103.4	14.8	70665	6	US-10-505-928-596
C 6	101.6	14.5	1615	8	US-11-266-748A-58095
C 7	100.4	14.3	1577	8	US-11-266-748A-25751
C 8	99.8	14.3	1000	8	US-11-266-748A-197923
C 9	99.8	14.3	8666	6	US-10-517-441-19
C 10	99.8	14.3	1237661	8	US-11-266-748A-29041
C 11	99.6	14.2	122568	8	US-11-266-748A-23292
C 12	99.2	14.2	1000	8	US-11-266-748A-205304
C 13	98.8	14.1	83965	6	US-10-539-228-826
C 14	98.8	14.1	110096	8	US-11-266-748A-61303
C 15	97.8	14.0	1000	8	US-11-266-748A-207140
C 16	97.8	14.0	301477	6	US-10-539-228-456
C 17	97.4	13.9	52987	6	US-10-539-228-386
C 18	97.2	13.9	638	8	US-11-266-748A-209478
C 19	97.2	13.9	301477	6	US-10-539-228-456
C 20	97	13.9	131546	8	US-11-266-748A-60109
C 21	96.8	13.8	1000	8	US-11-266-748A-290116
C 22	96.8	13.8	1000	8	US-11-266-748A-341545
C 23	96.8	13.8	261789	8	US-11-260-842-1
C 24	96.8	13.8	421987	8	US-11-266-748A-28210

ALIGNMENTS

RESULT 1  
US-11-266-748A-196825/c  
; Sequence 196825, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; PRIOR FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9

Sequence 117289,  
Sequence 159453,  
Sequence 288898,  
Sequence 340327,  
Sequence 398825,  
Sequence 470871,  
Sequence 3, Appli  
Sequence 232, App  
Sequence 29045, A  
Sequence 25123, A  
Sequence 204505,  
Sequence 60044, A  
Sequence 220785,  
Sequence 284468,  
Sequence 335897,  
Sequence 394477,  
Sequence 465523,  
Sequence 75, Appl  
Sequence 25150, A  
Sequence 60108, A  
Sequence 219620,  
Sequence 239532,  
Sequence 25123, A  
Sequence 86, Appl  
Sequence 87, Appl  
Sequence 28223, A  
Sequence 79, Appl  
Sequence 29045, A  
Sequence 23277, A  
Sequence 60144, A  
Sequence 50139, A  
Sequence 202832,  
Sequence 23474, A  
Sequence 23170, A  
Sequence 29041, A  
Sequence 200176,  
Sequence 60803, A  
Sequence 29039, A  
Sequence 211402,  
Sequence 37, Appl  
Sequence 59086, A  
Sequence 22833, A  
Sequence 200842,  
Sequence 25022, A  
Sequence 23809, A  
Sequence 60803, A

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; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 196825
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-196825

Query Match      15.8%; Score 110.8; DB 8; Length 1000;
Best Local Similarity 84.9%; Pred. No. 4.9e-11;
Matches 124; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 16 TTTTTCCTTTTCATGATGTTTATATAAAATATCATTTTCTCTTTTATATATATATACTT 75
Db 615 TTATTTTATTTTATTTTATTTTATTTTATTTTCTATTTTATTTTATATATATACTT 556

Qy 76 TTAAGTTTTAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135
Db 555 TTAAGTTTTAGGGTACATGTGTGCACAAATGTGCAGGTTAGTTACATATGTATACATGTGCCA 496

Qy 136 TCGTGTGTGCTGCACCCATTAACTC 161
Db 495 TCGTGTGTGCTGCACCCATTAACTC 470

RESULT 2
US-10-517-441-283
; Sequence 283, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 283
; LENGTH: 8666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-283

Query Match      15.2%; Score 106.6; DB 6; Length 8666;

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Best Local Similarity 49.0%; Pred: No. 3.2e-10;	
Matches 312; Conservative	0; Mismatches 324; Indels 1; Gaps 1;
Qy	12 AAAGTTTTTTTTTTTTTGATGATTTTAAATAAAATATCATTTTCTTTTTTATTTATTTAT 71
Db	1547 AAAGTTTTTTTTTTATTTATTAATTTATTTATATAAATATTTTTTAAATTTTATTTATTTA 1606
Qy	72 ACTTTTAAAGTTTTAGGGTACATGTCGAAAGTGTGCAGGTAGTTACATATATATACATGTT 131
Db	1607 TATTTTTAAAGTTTTAGAGTATATGTGTATATGTTAGGTTTGTATATATATGATATATGT 1666
Qy	132 GCCATGCTGCTGCTGTCGCCACCACTTAACATCAATGAAGTTTTTTTTTAAATTTTTAGTGACA 191
Db	1667 GTTATGTTGGTGTGTTATTTATTAATTTA-TTATTTAGTATTTAGGTATATTTTTTAAAT 1725
Qy	192 GTTTTGTAGTCATTTTCCCTAAATTTGAAAGTATCATTAAGTAATCCATAAAATTTGAAAAAATGT 251
Db	1726 GTTATTTTTTTTTTTTTTTTTTTTATATAAGATTTTATAATGGATAAATGGATTTTTTAAATTTT 1785
Qy	252 TAACTACTCTGTATAAAAAGTTTTTATAGTTTCCCTACTTTTAAAGCAAAATTTCCCATAGGGCA 311
Db	1786 AGAGTAAATGGTTTTTATTTAAGGATGTTATAAATTTTTTTAGAGTTTTTATGTAAGATAT 1845
Qy	312 TGTAAATGTGAGTTTCAACATTACTTTGCAGTTTTCAGTTAGTAAATAAATTAATTAAGCCTAG 371
Db	1846 GAGATATATATATTTAAAAATTTGTTTTTGGTATTTTAAAGTAGTTAAATTTTTTATATTTG 1905
Qy	372 TAAGTATAATTTAATATTTGTCAAATAATTTGGAAATACCATGGGTACTTAAATTGATTTT 431
Db	1906 TTTATATGATTTTAAATGTGTGTTTTATATGTTGTATTTTTTATTTTTTTTATTTAATA 1965
Qy	432 ACCAAATTTTCCATGGAAACAAACAAAGGTTCGCTATTTTTTTGGATTTGATATTTTGAAATACT 491
Db	1966 GTTATATATATTTTTTTTAAAGAGTTTCAAAGAGTTTTTTGATGTAGGAATTTTATGCTAGAGT 2025
Qy	492 AGTACAGGAATATCATGTTGATTTGAAATTTTACCCTTAGAAACAATGGAGTTTAGAT 551
Db	2026 TTTAGAGAAATTTTTTGAATTTATTTGAAAGTTTTTTTATTTAGAAATATATGTGTAAGTGAATA 2085
Qy	552 AGCTAAAGTATAATTTATTTTGTGATTTTAAATTAATGGTATGGAGTTAGGGCTATGATTAATTA 611
Db	2086 TATTTTTTTTAAAAAAATTTATTTATTTTTTTTTTTTGGAGAAGAGGTATTTATTTT 2145
Qy	612 GTGAAACACCCGAAGATGTTTTTATACTTTTTAAATTT 648
Db	2146 ATAGATTTTTTGAAGGAGTTTATTTTTTTTTTTTTTTT 2182
RESULT 3	
US-10-517-441-557	
; Sequence 557, Application US/10517441	
; Publication No. US20060121467A1	
; GENERAL INFORMATION:	
; APPLICANT: FOSKENS, John	
; APPLICANT: HARBECK, Nadia	
; APPLICANT: KOENIG, Thomas	
; APPLICANT: MAIER, Sabine	
; APPLICANT: MARTENS, John	
; APPLICANT: MODEL, Fabian	
; APPLICANT: NIMMRICH, Inko	
; APPLICANT: RUJAN, Tamas	
; APPLICANT: SCHMITT, Armin	
; APPLICANT: SCHMITT, Manfred	
; APPLICANT: LOCK, Maxime P.	
; APPLICANT: MARX, Almuth	
; APPLICANT: HOEFER, Heinz	
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of	
; TITLE OF INVENTION: proliferative disorders	
; FILE REFERENCE: 47675-93	
; CURRENT APPLICATION NUMBER: US/10/517, 441	
; PCT FILING DATE: 2004-12-11	
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881	
; PRIOR FILING DATE: 2003-10-01	

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; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 557
; LENGTH: 8666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-557

Query Match      15.2%; Score 106.6; DB 6; Length 8666;
Best Local Similarity 49.0%; Pred. No. 3.2e-10;
Matches 312; Conservative 0; Mismatches 324; Indels 1; Gaps 1;

Qy 12 AAAGTTTTTTTTTTTGGATGATTTTAATAAAATATCATTTTCTTTTTTATTATTAT 71
Db 1547 AAAGTTTTTTTATTATTATTAAATTTATATATATTTTAAATTTTATTATTATTA 1606

Qy 72 ACTTTTAAGTTTGGGTACATGTGCAAAAGTGCAGGTTAGTTACATATATATACATGT 131
Db 1607 TATTTTAAGTTTGAAGTATATGTGTATAATGTGTAGGTTTGGTTATATATATATATGT 1666

Qy 132 GCCATGCTGTGTGCTGCACCCATTAACTCACATCACTCACTCACTCACTCACTCACT 191
Db 1667 GTTATGTTGGGTGTGTGTATTTTAAATTTA-TTATTTAGTATTAGGTATATATTTTAAAT 1725

Qy 192 GTTTTAGTCATTTTCTCAATTTGAAAGTATCATAGTAATCCATAAATTTGAAAAAATGT 251
Db 1726 GTTATTTTCTTTTCTTTTATATAAGATTTTATATAGTATGATGATTTTAAATTTT 1785

Qy 252 TAACACTCTGATAAAAAGTTTATAGTTTTCCTACTTTTAAAGCAAAATCCATAGGGCA 311
Db 1786 AGAGTAAATGGTTTATTTAAGGATGTATATAATTTTGTAGAGTTTATTTGTAAGATAT 1845

Qy 312 TGGTAATGTAGTTTCAACATTAAGTTTGCAGTTTTCAGTTAGTTAAATAATTAAGCCTAG 371
Db 1846 GAGATATATATATTTAAATTTTGTGTTTGGTATTTTAAAGTAGTAAATTTTATATTTG 1905

Qy 372 TAAGTATAAATTAATTTGTCAAATAATTTGCAAAATACCATGGTACTTAATGATTTT 431
Db 1906 TTTTATATGATTTTAAAGTTGTTTATATAGTTGTATTTTATTTTATTATTATTAATA 1965

Qy 432 ACCAAATTTCCATGGAACAAACAAGTTGGCTATTTTGGATTTGATATTTTGAATACT 491
Db 1966 GTTATATATATATTTTATAAGAGTTGAAAGAGTTTTCATGTAGGAATTTATGGTAGAGT 2025

Qy 492 AGTACAGGAATATCATTTGTTAGTTGAATTTTTCAGCTTAGAAAACAATGGAGTTAGAT 551
Db 2026 TTTTAGAGAAATTTTGTGAATTTATTGAAAGTTTATTTTAGAATAATATATGTGTGAAGTGAATA 2085

Qy 552 AGCTAAAGTATAAATTTATTTCTGATTTTAAATGATGATGGAGTTAGGCTATGATAATTA 611
Db 2086 TATTTTATTAAAAAATTAATTTATTTTATTTTATTTTATTTTGGAGAAGGATTTATTATTTTA 2145

Qy 612 GTGAAACACCCCAAGATGTTTTTATACTTTTTAAATTT 648
Db 2146 ATAGATTTTGAAGGAGTTTATTTTATTTTATTTT 2182

RESULT 4
US-10-539-228-214
; Sequence 214, Application US/10539228
; Publication No. US20060154250A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: CHIR0052-101 (PP023370.0003)
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; CURRENT APPLICATION NUMBER: US/10/539,228
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 72678
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-539-228-214

Query Match      14.9%; Score 104.6; DB 6; Length 72678;
Best Local Similarity 80.8%; Pred. No. 8.7e-10;
Matches 122; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 11 TAAAGTTTTTTTTTTTGGATGATTTTAAATAAAATATCATTTTCTTTTTTATTATTATTA 70
Db 68541 TACAGAACTCTTTTTTTTTTTTTTTTTCATTTCTCTCTATATATATTTTATTATTATTA 68600

Qy 71 TACTTTTAAAGTTTGTAGGTACATGTGCAAAAGTGTGCAAGTTAGTTACATATATATACATG 130
Db 68601 TACTTTTAAAGTTTGTAGGTACATGTGCAAAAGTGTGCAAGTTAGTTACATATATATACATG 68660

Qy 131 TGCCATGCTGTGTGCTGCACCCATTAACTC 161
Db 68661 TGCCATGCTGTGTGCTGCACCCCTAACTC 68691

RESULT 5
US-10-505-928-596
; Sequence 596, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 596
; LENGTH: 70665
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-505-928-596

Query Match      14.8%; Score 103.4; DB 6; Length 70665;
Best Local Similarity 87.6%; Pred. No. 1.4e-09;
Matches 113; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 33 TTTTAAATAAATAATCATTTTCTTTTTTATTATTATTATTTTAAAGTTTACGGGTACA 92
Db 62754 TTTTCTTTTGGAGTTTCTTTTTTTTAAATATTATTATATCTTTTAAAGTTTACGGGTACA 62813

Qy 93 TGTGCAAGTGTGCAAGTTAGTTACATATATATACATGTGCCATGCTGCTGCTGCACCC 152
Db 62814 TGTGCAAAATGTGCAAGTTAGTTACATATATATATATATATATATATATATATATAT 62873

Qy 153 CATTAACCTC 161
Db 62874 CATTAACCTC 62882

RESULT 6
US-11-266-748A-58095/c
; Sequence 58095, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
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; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58095
; LENGTH: 1615
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-58095
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Query Match 14.5%; Score 101.6; DB 8; Length 1615;
Best Local Similarity 86.1%; Pred. No. 2.1e-09;
Matches 124; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 18 TTTTCTTTTTCATGATTTTAAATAATATCATTTCTTTTTTATTATTATATCTTT 77
Db 1615 TTTTCTTTTTCATGATTTTAAATAATATCATTTCTTTTTTATTATTATATCTTT 1557

QY 78 AAGTTTTCAGGTACATGCGAAGTGTGCAGGTAGTTACATATATATATATGCGCATG 137
Db 1556 AAGTTTTCAGGTACATGCGAAGTGTGCAGGTAGTTACATATATATATATGCGCATG 1497

QY 138 CTGCTGTGCTGCCACCCCAATTAATC 161
Db 1496 CTGCTGTGCTGCCACCCCAATTAATC 1473
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RESULT 7
US-11-266-748A-25751/c
; Sequence 25751, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
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; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25751
; LENGTH: 1577
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-25751

Query Match 14.3%; Score 100.4; DB 8; Length 1577;
Best Local Similarity 84.9%; Pred. No. 3.4e-09;
Matches 124; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 16 TTTTCTTTTTCATGATTTTAAATAATATCATTTCTTTTTTATTATTATATCTTT 75
Db 1573 TTTTCTTTTTCATGATTTTAAATAATATCATTTCTTTTTTATTATTATATCTTT 1515

QY 76 TTAAGTTTTCAGGTACATGCGAAGTGTGCAGGTAGTTACATATATATATATGCGCA 135
Db 1514 TTAAGTTTTCAGGTACATGCGAAGTGTGCAGGTAGTTACATATATATATATGCGCA 1455

QY 136 TGCTGTGCTGCCACCCCAATTAATC 161
Db 1454 TGCTGTGCTGCCACCCCAATTAATC 1429
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RESULT 8
US-11-266-748A-197923
; Sequence 197923, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 197923
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-197923
```

```
Query Match 14.3%; Score 99.8; DB 8; Length 1000;
Best Local Similarity 73.1%; Pred. No. 4.1e-09;
Matches 128; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 2 TGTTCACATAAAGTTTCTTTTTCATGATTTTAAATAATATCATTTCTTTTCTTTTA 61
Db 421 TGTTCAGTAAAGTCTGTTTCTTTTTCATGATTTTAAATAATATCATTTCTTTTCTTTT 480
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; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23292
; LENGTH: 122568
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23292

Query Match      14.2%; Score 99.6; DB 8; Length 122568;
Best Local Similarity 81.0%; Pred. No. 6.8e-09;
Matches 128; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

Qy   4   TTTCACATAAGTTTCTTTTTTTTGATGATTTTAATAAAATACATTTCTTTTATT 63
Db   6943 TTTATTCTTATTTTTTTTCTTTTTTTTTTTTAGTGTTCCTTTTTTTTCTTTT 6902

Qy   64   ATTATTATACTTTAAAGTTTITAGGGTACATCTGCAAAAGTGTGCAGGTTAGTTACATAT 123
Db   6903 ATTATTATAC-TTTAAGTTTITAGGGTACATCTGCGACATTTGTGCAGGTAGTTACATATG 6961

Qy   124   ATACATGTGCCATGCTGGTGTGCTGCACCCCATTAACTC 161
Db   6962 ATACATGTGCCACGCTGGTGTGCTGCACCCCAACTAACTC 6999

RESULT 12
US-11-266-748A-205304
; Sequence 205304, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266.748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 205304
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-205304

Query Match      14.2%; Score 99.2; DB 8; Length 1000;
Best Local Similarity 76.2%; Pred. No. 5.2e-09;
Matches 122; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy   2   TGTTTCACATAAAGTTTCTTTTTTTTGATGATTTTAATAAAATACATTTCTTTTATA 61
Db   609   TGTTACATTGTGATGATTTCTTTTTTTTATTTACTATTTATTTTATTATTATTT 668

Qy   62   TTATTATTACTTTTAAAGTTTTTAGGGGTACATGTGCAAAGTGTGCAGGTAGTTTACATAT 121
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; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61303
; LENGTH: 110096
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-61303

Query Match      14.1%; Score 98.8; DB 8; Length 110096;
Best Local Similarity 84.2%; Pred. No. 9.4e-09;
Matches 123; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

Qy   16  TTTTTCCTTTTTTGATGATTTTAATAAAATACATTCTTCTTTTATATATATATACTT 75
Db   16  TTTTTCCTTTTTTTGGCCTTCAAAAAGTTTATTTTATTTTATTTTATTTATATAC-T 104893

Qy   76  TTAAAGTTTTAGGTGCATGTGCAAAAGTGTGCAGGTAGTTCATCATATATACATGTGCCA 135
Db   76  TTAAGTTTTAGGTGACTTGTGCACACGTGCGAGGTGTTGTACATATGTNACATGTGCCA 104953

Qy   136  TGCTGGTGTGCTGCCACCCATTAACTC 161
Db   136  TGTTGGTGTGCTGCCACCCATTAACTC 104979

RESULT 15
US-11-266-748A-207140
; Sequence 207140, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 207140
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-207140

Query Match      14.0%; Score 97.8; DB 8; Length 1000;
Best Local Similarity 84.1%; Pred. No. 9.2e-09;
Matches 122; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

Qy   17  TTTTTCCTTTTTTGATGATTTTAATAAAATACATTCTTCTTTTATATATATATACTT 76

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; LENGTH: 131546  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-60109

Query Match 13.9%; Score 97; DB 8; Length 131546;  
Best Local Similarity 75.2%; Pred. No. 2e-08;  
Matches 121; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 CTTGTTCCATAAAGTTTTTTTTTTTGGATGATTTTAAATAATATCATTTCTTTTTTT 60  
DB 91001 CAGTCTAGTACAAACCGAAGTGTAAATGCAATCAATAGTTTCTTTTTTAATTT 91060  
QY 61 ATTATTATTATCTTTTAAAGTTTAAAGGTACATGTGCAAGGTGCAGGTAGTTACATA 120  
DB 91061 TTTTAAATTATTTTAAAGTTTAAAGGTACATGTGCAAGGTGCAGGTAGTTACATA 91120  
QY 121 TATATACATGCGCATGCTGGTGCTGCACCCATTAACCTC 161  
DB 91121 TGTATACATGCGCATGCTGGTGCTGCACCCATTAACCTC 91161

RESULT 21

US-11-266-748A-290116  
; Sequence 290116, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 290116  
; LENGTH: 1000  
; TYPE: DNA

; ORGANISM: Homo Sapiens  
US-11-266-748A-290116

Query Match 13.8%; Score 96.8; DB 8; Length 1000;  
Best Local Similarity 79.4%; Pred. No. 1.4e-08;  
Matches 127; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY 2 TGTTCACATAAAGTTTTTTTTTTTGGATGATTTTAAATAATATCATTTCTTTTTTTA 61  
DB 443 TGTATATAAAACCGTTTATTTCTCTATTACATATCTCTTTTCTTGTTTTTA 502  
QY 62 TTATTATTATCTTTTAAAGTTTAAAGGTACATGTGCAAGGTGCAGGTAGTTACATAT 121  
DB 503 TTATTATTATAC-TTTAAGTTTAAAGGTACATGTGCAAGGTGCAGGTAGTTACATAT 561  
QY 122 ATATACATGCGCATGCTGGTGCTGCACCCATTAACCTC 161  
|||||

DB 562 GTATACATGTGCCATATTGGTGCTGCACCCATTAACCTC 601

RESULT 22

US-11-266-748A-341545/c  
; Sequence 341545, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 341545  
; LENGTH: 1000  
; TYPE: DNA

; ORGANISM: Homo Sapiens  
US-11-266-748A-341545

Query Match 13.8%; Score 96.8; DB 8; Length 1000;  
Best Local Similarity 79.4%; Pred. No. 1.4e-08;  
Matches 127; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY 2 TGTTCACATAAAGTTTTTTTTTTTGGATGATTTTAAATAATATCATTTCTTTTTTTA 61  
DB 558 TGTATATAAAACCGTTTATTTCTCTATTACATATCTCTTTTCTTGTTTTTA 499  
QY 62 TTATTATTATCTTTTAAAGTTTAAAGGTACATGTGCAAGGTGCAGGTAGTTACATAT 121  
DB 498 TTATTATTATAC-TTTAAGTTTAAAGGTACATGTGCAAGGTGCAGGTAGTTACATAT 440  
QY 122 ATATACATGCGCATGCTGGTGCTGCACCCATTAACCTC 161  
DB 439 GTATACATGTGCCATATTGGTGCTGCACCCATTAACCTC 400  
|||||

RESULT 23

US-11-266-842-1/c  
; Sequence 1, Application US/11260842  
; Publication No. US20060115845A1  
; GENERAL INFORMATION:

; APPLICANT: Vance, Jeffrey M.  
; APPLICANT: Kraus, William E.  
; APPLICANT: Goldschmidt, Pascal J.  
; APPLICANT: Gregory, Simon G.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING GENETIC MARKERS WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE  
; FILE REFERENCE: 5405-347

; CURRENT APPLICATION NUMBER: US/11/260,842  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US 60/662,447  
; PRIOR FILING DATE: 2004-10-27

; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 261789  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-260-842-1

Query Match 13.8%; Score 96.8; DB 8; Length 261789;  
Best Local Similarity 84.0%; Pred. No. 2.3e-08;  
Matches 121; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

QY 17 TTTTCTTTTGGATGATTTTAAATAAATATCATTTCTTTTATATATATATATTT 76  
DB 257725 TTTTCTTTTGGAGTGCCTGAAGATTTTCAACTTTCTTTTATATATATAT 257667  
QY 77 TAAAGTTTAAAGGTACATGTGCAAGTGTGAGGTAGTTACATATATATACATGTGCCAT 136  
DB 257666 TAAAGTTTAAAGGTACATGTGCACAAATGTGAGGTAGTTACATATGTATACATGTGCCAT 257607  
QY 137 GCTGGTGTGCTGCACCCATTAAC 160  
DB 257606 GCGGGTGCCTGCACCCCACTAACT 257583

RESULT 24  
US-11-266-748A-28210/c  
; Sequence 28210, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Mulligan, Patrick  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; PRIOR FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 28210  
; LENGTH: 421987  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-28210  
Query Match 13.8%; Score 96.8; DB 8; Length 421987;  
Best Local Similarity 84.0%; Pred. No. 2.4e-08;  
Matches 121; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

QY 16 TTTTCTTTTGGATGATTTTAAATAAATATCATTTCTTTTATATATATATTT 75  
DB 48793 TTTTCTTTTGGTGTGTTGTTTAAATCTTTTATATATATATTTTATTTACTT 48734  
QY 76 TTAAGTTTAAAGGTACATGTGCAAGTGTGAGGTAGTTACATATATATACATGTGCCA 135  
DB 48733 -TAAAGTTTAAAGGTACATGTGCACAAATGTGAGGTAGTTACATATGTATACATGTGCCA 48675

QY 136 TGCTGGTGTGCTGCACCCATTAAC 159  
DB 48674 TGCTGGTGTGCTGCACCCCACTAAC 48651

RESULT 25  
US-11-266-748A-117289/c  
; Sequence 117289, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; PRIOR FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 117289  
; LENGTH: 1000  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-117289

Query Match 13.8%; Score 96.4; DB 8; Length 1000;  
Best Local Similarity 78.8%; Pred. No. 1.6e-08;  
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 16 TTTTCTTTTGGATGATTTTAAATAAATATCATTTCTTTTATATATATTT 75  
DB 986 TTTTCTTTTGGATGATTTTAAATAAATATCATTTCTTTTATATATTTACT 927  
QY 76 TTAAGTTTAAAGGTACATGTGCAAGTGTGAGGTAGTTACATATATATACATGTGCCA 135  
DB 926 TTAAGTTTAAAGGTACATGTGCACAACTGTGAGGTAGTTACATATGTATACATGTGCCA 867  
QY 136 TGCTGGTGTGCTGCACCCATTAAC 161  
DB 866 TGCTGGTGTGCTGCACCCCACTAAC 841

RESULT 26  
US-11-266-748A-159453  
; Sequence 159453, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03

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; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 159453
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-159453

Query Match      13.8%; Score 96.4; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 16 TTTTCTTTTGTGATGATTTTAAATAAATATATCATTTCTTTTATTTATTTATTTACTT 75
Db 15 TTTTCTTTTGTGATGATTTTAAATAAATATATCATTTCTTTTATTTATTTATTTACTT 74
Qy 76 TTAAGTTTGTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 135
Db 75 TTAAGTTTGTAGGTACATGTGCACACGTGCGAGTTGTACATATGTATACATGTGCCA 134
Qy 136 TCGTGGTGTGCTGCCACCCATTAACTC 161
Db 135 TGGTGGTGTGCTGCCACCCATTAACTC 160

RESULT 27
US-11-266-748A-288898/c
; Sequence 288898, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 288898
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-288898
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; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-288898

Query Match      13.8%; Score 96.4; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 16 TTTTCTTTTGTGATGATTTTAAATAAATATATCATTTCTTTTATTTATTTATTTACTT 75
Db 986 TTTTCTTTTGTGATGATTTTAAATAAATATATCATTTCTTTTATTTATTTATTTACTT 927
Qy 76 TTAAGTTTGTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 135
Db 926 TTAAGTTTGTAGGTACATGTGCACACGTGCGAGTTGTACATATGTATACATGTGCCA 867
Qy 136 TCGTGGTGTGCTGCCACCCATTAACTC 161
Db 866 TGGTGGTGTGCTGCCACCCATTAACTC 841

RESULT 28
US-11-266-748A-340327
; Sequence 340327, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 340327
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-340327

Query Match      13.8%; Score 96.4; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 16 TTTTCTTTTGTGATGATTTTAAATAAATATATCATTTCTTTTATTTATTTATTTACTT 75
Db 15 TTTTCTTTTGTGATGATTTTAAATAAATATATCATTTCTTTTATTTATTTATTTACTT 74
Qy 76 TTAAGTTTGTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 135
Db 75 TTAAGTTTGTAGGTACATGTGCACACGTGCGAGTTGTACATATGTATACATGTGCCA 134
Qy 136 TCGTGGTGTGCTGCCACCCATTAACTC 161
Db 135 TGGTGGTGTGCTGCCACCCATTAACTC 161
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Db      135 TGGTGGTGTGTCGACCCATTAACTC 160
;
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 470871
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-470871

Query Match      13.8%; Score 96.4; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY      16 TTTTCTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 75
Db      15 TTTTCTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 74
QY      76 TTAAGTTTTCAGGTACATGTGCAAAAGTGCAGGTTAGTTACATATATACATGTGCCA 135
Db      75 TTAAGTTTTCAGGTACATGTGCACACGTCGAGGTTGTACATATGTACATGTGCCA 134
QY      136 TGCTGGTGTGCTGCACCCATTAACTC 161
Db      135 TGGTGGTGTGCTGCACCCATTAACTC 160

RESULT 31
US-10-506-549-3
; Sequence 3, Application US/10506549
; Publication No. US20060100417A1
; GENERAL INFORMATION:
; APPLICANT: APPLERA CORPORATION
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001361-US
; CURRENT APPLICATION NUMBER: US/10/506,549
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/361,343
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 394191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(394191)
; OTHER INFORMATION: n = A,T,C or G
US-10-506-549-3

Query Match      13.8%; Score 96.4; DB 6; Length 394191;
Best Local Similarity 78.8%; Pred. No. 2.8e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY      16 TTTTCTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 75
Db      136948 TTTTCTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 137007
QY      76 TTAAGTTTTCAGGTACATGTGCAAAAGTGCAGGTTAGTTACATATATACATGTGCCA 135
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Db      135 TGGTGGTGTGTCGACCCATTAACTC 160
;
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 399825
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-399825

Query Match      13.8%; Score 96.4; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY      16 TTTTCTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 75
Db      986 TTTTCTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTACTT 927
QY      76 TTAAGTTTTCAGGTACATGTGCAAAAGTGCAGGTTAGTTACATATATACATGTGCCA 135
Db      926 TTAAGTTTTCAGGTACATGTGCACACGTCGAGGTTGTACATATGTACATGTGCCA 867
QY      136 TGCTGGTGTGCTGCACCCATTAACTC 161
Db      866 TGGTGGTGTGCTGCACCCATTAACTC 841

RESULT 30
US-11-266-748A-470871
; Sequence 470871, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
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;  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 48396  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 220785  
; LENGTH: 1000  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-220785

Query Match 13.6%; Score 95.2; DB 8; Length 1000;  
Best Local Similarity 82.9%; Pred. No. 2.6e-08;  
Matches 121; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

Qy 18 TTTTGTGATGATGTTTAAATAATATCATTTTCTTTTATTTATTTATTTATTTACT--T 75  
Db 465 TTGTGTTATTTATTTATTTTAAATTTTAAATTTTATTTATTTATTTATTTATTTACT 524

Qy 76 TTAAGTTTATAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135  
Db 525 TTAAGTTTATAGGTACATGTGCACATGTGCAGGTTAGTTACATATGTATACATGTGCCA 584

Qy 136 TGCTGGTGTGCTGCACCCATTAACTC 161  
Db 585 TGCTGGTGTGCTGCACCCATTAACTC 610

RESULT 38  
US-11-266-748A-284468  
; Sequence 284468, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 48396  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 284468  
; LENGTH: 1000  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-284468

Query Match 13.6%; Score 95.2; DB 8; Length 1000;  
Best Local Similarity 82.9%; Pred. No. 2.6e-08;  
Matches 121; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

Qy 18 TTTTGTGATGATGTTTAAATAATATCATTTTCTTTTATTTATTTATTTATTTACT--T 75  
Db 465 TTGTGTTATTTATTTATTTTAAATTTTAAATTTTATTTATTTATTTATTTATTTACT 524

Qy 76 TTAAGTTTATAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135  
Db 525 TTAAGTTTATAGGTACATGTGCACATGTGCAGGTTAGTTACATATGTATACATGTGCCA 584

Qy 136 TGCTGGTGTGCTGCACCCATTAACTC 161  
Db 585 TGCTGGTGTGCTGCACCCATTAACTC 610

RESULT 39  
US-11-266-748A-335897/c  
; Sequence 335897, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 48396  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 335897  
; LENGTH: 1000  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-335897

Query Match 13.6%; Score 95.2; DB 8; Length 1000;  
Best Local Similarity 82.9%; Pred. No. 2.6e-08;  
Matches 121; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

Qy 18 TTTTGTGATGATGTTTAAATAATATCATTTTCTTTTATTTATTTATTTATTTACT--T 75  
Db 536 TTGTGTTATTTATTTATTTTAAATTTTAAATTTTATTTATTTATTTATTTATTTACT 477

Qy 76 TTAAGTTTATAGGTACATGTGCAAGTGTGCAGGTTAGTTACATATATATACATGTGCCA 135  
Db 476 TTAAGTTTATAGGTACATGTGCACATGTGCAGGTTAGTTACATATGTATACATGTGCCA 417

Qy 136 TGCTGGTGTGCTGCACCCATTAACTC 161  
Db 416 TGCTGGTGTGCTGCACCCATTAACTC 391

RESULT 40  
US-11-266-748A-394477  
; Sequence 394477, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 48396  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 394477  
; LENGTH: 1000  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-394477

Query Match 13.6%; Score 95.2; DB 8; Length 1000;  
Best Local Similarity 82.9%; Pred. No. 2.6e-08;  
Matches 121; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

Qy 18 TTTTGTGATGATGTTTAAATAATATCATTTTCTTTTATTTATTTATTTATTTACT--T 75  
Db 465 TTGTGTTATTTATTTATTTTAAATTTTAAATTTTATTTATTTATTTATTTATTTACT 524

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; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662, 276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700, 293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 394477
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-394477
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Query Match      13.6%; Score 95.2; DB 8; Length 1000;
Best Local Similarity 82.9%; Pred. No. 2.6e-08;
Matches 121; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

QY      18  TTTTCTTTTGGATGATTTTAAATAAATATCATCTTTCTTTTATTTATTTATTTACT--T 75
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      465  TTGTTTATTATTATTATTTTAAATTTTAAATTTTATTTATTTATTTATTTACT 524

QY      76  TTAAGTTTGGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATATATACATGTGCCA 135
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      525  TTAAGTTTGGGTACATGTGCACATGTGCAGGTTAGTTACATATGTATACATGTGCCA 584

QY      136  TGTGTGTGCTGCACCCATTAACTC 161
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      585  TGTGTGTGCTGCACCCATTAACTC 610
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RESULT 41
US-11-266-748A-465523/c
; Sequence 465523, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662, 276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700, 293
; PRIOR FILING DATE: 2005-07-18
```

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; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 465523
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-465523

Query Match      13.6%; Score 95.2; DB 8; Length 1000;
Best Local Similarity 82.9%; Pred. No. 2.6e-08;
Matches 121; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

QY      18  TTTTCTTTTGGATGATTTTAAATAAATATCATCTTTCTTTTATTTATTTATTTACT--T 75
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      536  TTGTTTATTATTATTATTTTAAATTTTAAATTTTATTTATTTATTTATTTACT 477

QY      76  TTAAGTTTGGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATATATACATGTGCCA 135
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      476  TTAAGTTTGGGTACATGTGCACAAATGTGCAGGTTAGTTACATATGTATACATGTGCCA 417

QY      136  TGTGTGTGCTGCACCCATTAACTC 161
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      416  TGTGTGTGCTGCACCCATTAACTC 391
```

```
RESULT 42
US-11-347-766-75/c
; Sequence 75, Application US/11347766
; Publication No. US20060134751A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F
; APPLICANT: Liang, Yinghua
; TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
; TITLE OF INVENTION: Hematopoietic Cells
; FILE REFERENCE: 180/132 PCT/US
; CURRENT APPLICATION NUMBER: US/11/347,766
; CURRENT FILING DATE: 2006-02-02
; PRIOR APPLICATION NUMBER: US/10/433,287
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 22884
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: genomic DNA
; LOCATION: (1)..(22884)
; OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, or dTTP)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9562)..(9621)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: initial coding region
; LOCATION: (12238)..(12393)
; FEATURE:
; NAME/KEY: coding_region
; LOCATION: (13544)..(13681)
; FEATURE:
; NAME/KEY: coding region
; LOCATION: (15338)..(15394)
; FEATURE:
; NAME/KEY: coding_region
; LOCATION: (18027)..(18188)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18413)..(18436)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: coding_region
; LOCATION: (19594)..(19695)
; FEATURE:
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Db 18938 GTTTTTTTTCCCTGTTTCCCTCACTCTCTTTTTTTTTTTCTTTTTTTTTTTTATTAT 18997

Qy 75 --TTTAAAGTTTGGGTACATGTCAAAGTGTGCAGGTTAGTTACATATATATACATG 132

Db 18998 ACTTTAAGTTTGGGTACATGTCACCTTGTGCAGGTTAGTTACATATGTTACATG 19057

Qy 133 CCACTGCTGCTGTGCTGCACCCCACTTAAC 161

Db 19058 CCACTGCTGCTGCTGCACCCCACTTAAC 19086

RESULT 48

US-11-175-714-86

; Sequence 86, Application US/11175714

; Publication No. US20060122373A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals, Inc.

; APPLICANT: McCarthy, Sean A.

; APPLICANT: Gearing, David

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Pan, Yang

; APPLICANT: Busfield, Samantha J.

; APPLICANT: Barnes, Thomas M.

; APPLICANT: Mackay, Charles

; APPLICANT: Lora, Jose M.

; TITLE OF INVENTION: DELTA3, FTHMA-070, TANGO85, TANGO77,

; TITLE OF INVENTION: SPOIL, NEOKINE, TANGO129 AND INTEGRIN ALPHA SUBUNIT PROTEIN

; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES AND USES THEREOF

; FILE REFERENCE: MPI05-0100NM1

; CURRENT APPLICATION NUMBER: US/11/175,714

; CURRENT FILING DATE: 2005-07-05

; PRIOR APPLICATION NUMBER: US 10/417,719

; PRIOR FILING DATE: 2003-04-17

; PRIOR FILING DATE: 2000-05-09

; PRIOR FILING DATE: 1997-06-11

; PRIOR FILING DATE: 2003-04-17

; PRIOR FILING DATE: 1997-06-11

; PRIOR FILING DATE: 2004-07-21

; PRIOR FILING DATE: 1997-04-04

; PRIOR FILING DATE: 2004-07-21

; PRIOR FILING DATE: 1997-04-04

; PRIOR FILING DATE: 2002-03-25

; PRIOR FILING DATE: 2002-03-25

; PRIOR FILING DATE: 2001-05-22

; PRIOR FILING DATE: 1998-04-17

; PRIOR FILING DATE: 1997-10-10

; PRIOR FILING DATE: 1997-04-18

; PRIOR FILING DATE: 1997-04-18

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 195

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 86

; LENGTH: 152331

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (1)...(152331)

; OTHER INFORMATION: n = A,T,C or G

US-11-175-714-86

Query Match 13.6%; Score 95; DB 8; Length 152331;

Best Local Similarity 76.8%; Pred. No. 4.5e-08;

Matches 116; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 11 TAAAGTTTTTTTTTTCATGATTTTAAATAAATATCATTTCTTTTTTTTATTATTATTA 70

Db 135565 TATTTTATTTTATTTTATTTATTTATTTATTTTAAATTTTTTTTAAATTT 135624

Qy 71 TACTTTTAAAGTTTGGGTACATGTCAAAGTGTGCAGGTTAGTTACATATATATACATG 130

Db 135625 ATGCTTTTAAAGTTTGGGTACATGTCACATTTGTGCAGGTTAGTTACATACGCATACATG 135684

Qy 131 TGCATGCTGCTGTGCTGCACCCCACTTAAC 161

Db 135685 CGCCATGCTGCTGTGCTGCACCCCACTTAAC 135715

RESULT 49

US-11-175-714-87

; Sequence 87, Application US/11175714

; Publication No. US20060122373A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals, Inc.

; APPLICANT: McCarthy, Sean A.

; APPLICANT: Gearing, David

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Pan, Yang

; APPLICANT: Busfield, Samantha J.

; APPLICANT: Barnes, Thomas M.

; APPLICANT: Mackay, Charles

; APPLICANT: Lora, Jose M.

; TITLE OF INVENTION: DELTA3, FTHMA-070, TANGO85, TANGO77,

; TITLE OF INVENTION: SPOIL, NEOKINE, TANGO129 AND INTEGRIN ALPHA SUBUNIT PROTEIN

; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES AND USES THEREOF

; FILE REFERENCE: MPI05-0100NM1

; CURRENT APPLICATION NUMBER: US/11/175,714

; CURRENT FILING DATE: 2005-07-05

; PRIOR APPLICATION NUMBER: US 10/417,719

; PRIOR FILING DATE: 2003-04-17

; PRIOR APPLICATION NUMBER: US 09/568,218

; PRIOR FILING DATE: 2000-05-09

; PRIOR APPLICATION NUMBER: US 09/872,855

; PRIOR FILING DATE: 1997-06-11

; PRIOR APPLICATION NUMBER: US 09/832,633

; PRIOR FILING DATE: 1997-04-04

; PRIOR APPLICATION NUMBER: US 10/895,676

; PRIOR FILING DATE: 2004-07-21

; PRIOR APPLICATION NUMBER: US 10/105,934

; PRIOR FILING DATE: 2002-03-25

; PRIOR APPLICATION NUMBER: US 09/862,972

; PRIOR FILING DATE: 2001-05-22

; PRIOR APPLICATION NUMBER: US 09/062,389

; PRIOR FILING DATE: 1998-04-17

; PRIOR APPLICATION NUMBER: US 60/062,017

; PRIOR FILING DATE: 1997-10-10

; PRIOR APPLICATION NUMBER: US 60/044,746

; PRIOR FILING DATE: 1997-04-18

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 195

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 87

; LENGTH: 176373

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (1)...(176373)

; OTHER INFORMATION: n = A,T,C or G

US-11-175-714-87

Query Match 13.6%; Score 95; DB 8; Length 176373;

Best Local Similarity 76.8%; Pred. No. 4.5e-08;

Matches 116; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 11 TAAAGTTTTTTTTTTCATGATTTTAAATAAATATCATTTCTTTTTTTTATTATTATTA 70

Db 148145 TATTTTATTTTATTTTATTTATTTATTTTAAATTTTTTTTAAATTT 148204

Qy 71 TACTTTTAAAGTTTGGGTACATGTCAAAGTGTGCAGGTTAGTTACATATATATACATG 130

Db 148205 ATGCTTTTAAAGTTTGGGTACATGTCACATTTGTGCAGGTTAGTTACATACGCATACATG 148264

```
QY 131 TGGCAGTCTGGTGTGCTGCACCCCACTTAATC 161
|||||
Db 148265 CGCCATGCTGGTGGCTGCACCCCACTTAATC 148295

RESULT 50
US-11-266-748A-28223
; Sequence 28223, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28223
; LENGTH: 495475
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14152)..(14163)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14173)..(14173)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20582)..(20681)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21980)..(21980)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21992)..(21992)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (42256)..(42256)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (42260)..(42260)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (42263)..(42263)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:

; NAME/KEY: misc feature
; LOCATION: (202648)..(202648)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202661)..(202661)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202663)..(202663)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202671)..(202671)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202680)..(202680)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202684)..(202684)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202686)..(202686)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202691)..(202691)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202696)..(202696)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202701)..(202701)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (202712)..(202712)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (448497)..(448497)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (448499)..(448500)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (448538)..(448538)
; OTHER INFORMATION: n is a, c, g, or t
; US-11-266-748A-28223

Query Match 13.6%; Score 95; DB 8; Length 495475;
Best Local Similarity 76.8%; Pred. No. 5e-08;
Matches 116; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 11 TAAAGTTTTTTTTTTTGATTTTAAATAAATATCATTTCTTTTTTATTATTATTA 70
Db 199353 TATTTATTTTTTATTTTATTTATTTATTTATTTTAAATTTTTTAAATTTTAAATTT 199412

QY 71 TACTTTTAAGTTTTAGGGTACATGTGCAAGTGTGAGGTTAGTTACATATATACATG 130
Db 199413 ATGCTTTAAGTTTTAGGGTACATGTGCACATTGTGCAGGTTAGTTACATACGCATACATG 199472

QY 131 TGGCATGCTGGTGTGCTGCACCCCACTTAATC 161
Db 199473 CGCCATGCTGGTGGCTGCACCCCACTTAATC 199503
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RESULT 51
US-11-347-766-79/c
; Sequence 79, Application US/11347766
; Publication No. US20060134751A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F
; APPLICANT: Llang, Yinghua
; TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
; FILE OF INVENTION: Hematopoietic Cells
; FILE REFERENCE: 180/132 PCT/US
; CURRENT APPLICATION NUMBER: US/11/347,766
; CURRENT FILING DATE: 2006-02-02
; PRIOR APPLICATION NUMBER: US/10/433,287
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 104644
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: genomic DNA
; LOCATION: (1)..(104644)
; OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(3)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (39)..(39)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (70)..(70)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (73)..(73)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (143)..(143)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (231)..(231)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (242)..(242)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (362)..(362)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11659)..(11659)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11699)..(11699)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: MS4A7 initial coding_region
; LOCATION: (17493)..(17639)
; FEATURE:
; NAME/KEY: MS4A7 coding region
; LOCATION: (19439)..(19573)
; FEATURE:
; NAME/KEY: MS4A7 coding region

```





```
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23474
; LENGTH: 347503
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23474

Query Match      13.4%; Score 93.8; DB 8; Length 347503;
Best Local Similarity 83.74; Pred. No. 7.8e-08;
Matches 118; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

Qy 21 TTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTATTATTATTATTAAAG 80
Db 334107 TTTTATTTTATTTTTCGACTCTTTTATTATTATTATTATTATTATAC-TTTAAG 334165

Qy 81 TTTTAGGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCATGCTG 140
Db 334166 TTTTAGGGTACAGTGCACATGTGCAGGTAGTTACATATGTATACATGTGCCATGCTG 334225

Qy 141 GTGTGCTGCACCACTTAACTC 161
Db 334226 GTGTGCTGCACCACTTAACTC 334246

RESULT 58
US-11-266-748A-23170
; Sequence 23170, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnstson, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 5815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23170
; LENGTH: 170452
; TYPE: DNA
; ORGANISM: Homo Sapiens
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; LOCATION: (3381)..(3381)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc feature
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; NAME/KEY: misc feature
; LOCATION: (3406)..(3407)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3423)..(3423)
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc feature
; LOCATION: (3907)..(3907)
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; NAME/KEY: misc feature
; LOCATION: (3909)..(3909)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc feature
; LOCATION: (3922)..(3922)
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; LOCATION: (3924)..(3924)
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; LOCATION: (3927)..(3927)
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; NAME/KEY: misc feature
; LOCATION: (15605)..(15605)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (144156)..(144156)
; OTHER INFORMATION: n is a, c, g, or t
; US-11-266-748A-23170

Query Match      13.4%; Score 93.6; DB 8; Length 170452;
Best Local Similarity 80.3%; Pred. No. 7.9e-08;
Matches 122; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

Qy 11 TAAAGTTTTTTTTTTTGGATGATTTTAAATAAATAATATCATTTCTTTTATTATTATTATTA 70
Db 122784 TAATCTTTTCTTAATTTCTACCAATTAATTTTCTTTTAAATTTTATTATTATTATTA 122843

Qy 71 TACTTTTAAAGTTTATAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATG 130
Db 122844 TAC-TTTAAGTTTTTATAGGTACATGTGCAATGTGCAGGTTTGTACATATGTATACATG 122902

Qy 131 TGCATGCTGGTGTGCTGCACCACTTAACCTCA 162
Db 122903 TGCCATGTTGGTGTGCTGCACCACTTAACCTCA 122934
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Query Match      13.3%; Score 93.2; DB 8; Length 176928;
Best Local Similarity 78.5%; Pred.No. 9.3e-08;
Matches 124; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 TTTTCACATAAGTTTTTTTTTTTGTGATGATTTTAAATAAAATATCATTTCTTTTTTATT 63
Db 102485 TTGCATAAAATCTTTTGTCTTCTGTTCTATTAATATATTTTCTTCTTCTTTTATT 102544

QY 64 ATTATTATACTTTAAAGTTTGTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATAT 123
Db 102545 ATTATTATAC-TTTAAAGATTAGGTACATGTGCACAATGTGCAGGTAGTTACATATGT 102603

QY 124 ATACATGTGCCATGCTGTGCTGTCGCCACCATTAACTC 161
Db 102604 AAACATGTGCCATGCTGTGCTGTCGCCACCATTAAC 102641

RESULT 62
US-11-266-748A-29039
; Sequence 29039, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29039
; LENGTH: 909203
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-29039

Query Match      13.3%; Score 93.2; DB 8; Length 909203;
Best Local Similarity 78.1%; Pred.No. 1.1e-07;
Matches 125; Conservative 0; Mismatches 33; Indels 2; Gaps 1;

QY 4 TTTTCACATAAGTTTTTTTTTTTGTGATGATTTTAAATAAAATATCATTTCTTTTTTATT 63
Db 255117 TTTACTATATTTTATTTTATTTTGTAAATTTTATTTTATTTTCTATGATTATTTT 255176

QY 64 ATTATTATAC-TTTAAAGTTTGTAGGTACATGTGCAAGTGTGCAGGTAGTTACATAT 121
Db 255177 ATTATTATATAC-TTTAAAGTTTGTAGGTACATGTGCAATGTGCAGGTAGTTACATAT 255236

QY 122 ATATACATGTGCCATGCTGTGCTGTCGCCACCATTAACTC 161
Db 255237 GTATACATGTGCCATGCTGTGCTGTCGCCACCATTAACTC 255276

RESULT 63
US-11-266-748A-211402
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; Sequence 211402, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 211402
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-211402

Query Match      13.3%; Score 93; DB 8; Length 607;
Best Local Similarity 94.7%; Pred.No. 6.1e-08;
Matches 107; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 49 TTTTCTTTTTTATTATTATTATTATATACTTTAAAGTTTGTAGGTACATGTGCAAGTGTGCAG 108
Db 4 TTTTCTTTTTTATTATTATTATTATATAC-TTTAAAGTTTGTAGGTACATGTGCAATGTGCAG 62

QY 109 GTTAGTTACATATATATACATGTGCCATGCTGTGCTGTCGCCACCATTAACTC 161
Db 63 GTTAGTTACATATGTATATACATGTGCCATGCTGTGCTGCTACACCATTAACTC 115

RESULT 64
US-10-519-335-37
; Sequence 37, Application US/10519335
; Publication No. US20060099210A1
; GENERAL INFORMATION:
; APPLICANT: Cavarec, Laurent
; APPLICANT: Chumakov, Ilya
; APPLICANT: Destenaves, Benoit
; APPLICANT: Gonthier, Catherine
; APPLICANT: Elias, Isabelle
; TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN THE
; FILE REFERENCE: G-194US03PCT
; CURRENT APPLICATION NUMBER: US/10/519,335
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 60/391,359
; PRIOR FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 151830
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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Oy 61 ATTATTATTATCTTTTAAAGTTTATAGGTACATGTGCAAGTGTCAGGTTAGTTACATA 120
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Db 61711 ATTATTATTATAC-TTTAAGTTTATAGGTACATGTGCAATGTGCAGGTTAGTTACATA 61769
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Oy 121 TATATACATGTGCCATGCTGGTGTCTGCACCCATTAACTC 161
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Db 61770 TGTATACAGGTGCCATGATGGTGTCTGTCATCCATTAACTC 61810

RESULT 67
US-11-266-748A-200842/c
; Sequence 200842, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; CURRENT APPLICATION NUMBER: US/11/266,748A
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 200842
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-200842

Query Match 13.3%; Score 92.8; DB 8; Length 1000;
Best Local Similarity 78.8%; Pred. No. 6.9e-08;
Matches 123; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

Oy 5 TTCACATAAAGTTTCTTTTGGTGTGATTTTAAATAAATATCATTTCTTTTATTATA 64
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Db 155 TTTAAACATTTTGTATGTATTTTAAATACAGGTTAGTTATTTCTTTTAAATTTA 96
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 65 TTATTATATCTTTTAAAGTTTATAGGTACATGTGCAAGTGTCAGGTTAGTTACATATATA 124
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 95 TTATTATAC-TTTAAGTTTATAGGTACATGTGCAATGTGCAGGTTAGTTACATATGTA 37
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Oy 125 TACATGTGCCATGCTGGTGTCTGCACCCATTAACT 160
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 36 TACATGTGCATGCTGGTGTCTGCACCCATTAACT 1

RESULT 68
US-11-266-748A-25022
; Sequence 25022, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
```

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; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25022
; LENGTH: 38399
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-25022

Query Match 13.3%; Score 92.8; DB 8; Length 38399;
Best Local Similarity 89.3%; Pred. No. 9.6e-08;
Matches 100; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 50 TTTCTTTTTTTTATTATTATTATCTTTTAAAGTTTATAGGTACATGTGCAAGTTGTCAGG 109
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 19144 TTTCTTTTTTTTAAATTTATCTTTTAAAGTTTATAGGTACATGTGTCAGG 19203
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Oy 110 TTAGTTACATATATATACATGTGCCATGCTGGTGTGTCACCCATTAACTC 161
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 19204 TTAGTTACATATGTATACATGTGCCATGCTGGTGTGTCACCCATTAACTC 19255
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RESULT 69
US-11-266-748A-23809
; Sequence 23809, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: July 19, 2006, 06:54:08 ; Search time 4403 Seconds  
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Title: US-10-661-966-1\_146001-146700\_A146311  
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Scoring table: IDENTITY.NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 70 summaries

Database :

EST:\*

- 1: gb\_est1:\*
- 2: gb\_est3:\*
- 3: gb\_est4:\*
- 4: gb\_est5:\*
- 5: gb\_est6:\*
- 6: gb\_hic:\*
- 7: gb\_est2:\*
- 8: gb\_est7:\*
- 9: gb\_est8:\*
- 10: gb\_est9:\*
- 11: gb\_gss1:\*
- 12: gb\_gss2:\*
- 13: gb\_gss3:\*
- 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110	15.7	961	4	BX415806
2	107.4	15.3	785	12	BZ598311 WHADR40TR
3	106.8	15.3	522	11	B52311 CIT-HSP-388
4	102.8	14.7	375	11	AQ356702 CITBI-E1-
5	102.8	14.7	632	11	AQ195233 RPCI11-48
6	102.6	14.7	567	9	DB349127 DB349127
7	102	14.6	397	11	AQ111354 CIT-HSP-2
8	102	14.6	506	9	CX869873 HESCA_38
9	102	14.6	552	9	DA104597 DA104597
10	101.8	14.5	421	11	AQ884211 HS_5499_B
11	101.8	14.5	681	14	AG102621 Pan trogl
12	101.4	14.5	591	11	AQ527159 CITBI-E1-
13	101.2	14.5	242	10	W44804 zB98G09.s1
14	101.2	14.5	527	11	AQ756779 HS_5407_A
15	100.8	14.4	445	13	CZ457195 MCF740G11
16	100.8	14.4	746	8	CR737970 CR737970
17	100.6	14.4	417	11	AQ021610 CIT-HSP-2
18	100.4	14.3	225	4	CB048927 NISC_G107
19	100.4	14.3	233	4	CB410332 NISC_nc11

20	100.4	14.3	285	11	AQ229797
21	100.4	14.3	451	11	AQ109589
22	100.4	14.3	541	1	AL310239
23	100.4	14.3	1577	6	BC010517 Homo sapi
24	100.2	14.3	572	11	B72257
25	100.2	14.3	671	14	CR59536
26	100.2	14.3	870	13	CZ450878
27	100	14.3	307	1	AA344409
28	100	14.3	621	4	CA947015
29	100	14.3	672	11	AQ052012
30	100	14.3	677	1	AL601657
31	99.6	14.2	272	11	AQ266524
32	99.4	14.2	352	14	AG189910
33	99.4	14.2	505	9	DA502536
34	99.4	14.2	548	11	B92240
35	99.4	14.2	771	3	BQ007697
36	99.4	14.2	906	3	BQ924499
37	99.2	14.2	571	11	AQ319769
38	99	14.1	401	1	AA446110
39	99	14.1	464	11	AQ029723
40	99	14.1	553	9	DB302517
41	99	14.1	665	14	AG042325
42	99	14.1	704	11	AQ779743
43	98.8	14.1	419	10	Z36956
44	98.8	14.1	424	11	AQ042547
45	98.8	14.1	468	11	AQ127855
46	98.8	14.1	561	11	AQ550918
47	98.8	14.1	725	3	BQ447264
48	98.8	14.1	853	13	CZ446241
49	98.8	14.1	3088	6	BC032464
50	98.4	14.1	324	11	AQ017761
51	98.4	14.1	398	11	AQ605001
52	98.4	14.1	713	4	BX115372
53	98.2	14.0	273	3	BUE07283
54	98.2	14.0	555	11	AZ519511
55	98.2	14.0	226	9	DB097926
56	98	14.0	263	3	BQ352132
57	98	14.0	480	11	AQ628311
58	98	14.0	740	14	CR958489
59	97.8	14.0	385	11	B75832
60	97.8	14.0	657	8	CR750736
61	97.8	14.0	724	11	AF118407
62	97.6	13.9	513	11	AQ464599
63	97.6	13.9	708	13	CZ465237
64	97.4	13.9	443	11	B72013
65	97.4	13.9	661	14	AG121371
66	97.4	13.9	712	13	CZ179389
67	97.4	13.9	725	12	BZ610242
68	97.4	13.9	995	6	CR597534
69	97.2	13.9	238	2	BF954789
70	97.2	13.9	256	1	AI570164

ALIGNMENTS

RESULT 1	BX415806	961 bp	linear	EST 03-MAY-2004
LOCUS	BX415806	961 bp	linear	EST 03-MAY-2004
DEFINITION	BX415806 Homo sapiens THYMUS Homo sapiens	961 bp	linear	EST 03-MAY-2004
ACCESSION	BX415806	961 bp	linear	EST 03-MAY-2004
KEYWORDS	BX415806.2	GI:46953996	linear	EST 03-MAY-2004
SOURCE	BX415806	961 bp	linear	EST 03-MAY-2004
ORGANISM	BX415806	961 bp	linear	EST 03-MAY-2004
REFERENCE	BX415806	961 bp	linear	EST 03-MAY-2004
AUTHORS	BX415806	961 bp	linear	EST 03-MAY-2004
TITLE	BX415806	961 bp	linear	EST 03-MAY-2004
JOURNAL	BX415806	961 bp	linear	EST 03-MAY-2004

Unpublished (2001)

## COMMENT

On May 15, 2003 this sequence version replaced gi:30765544.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 1683.f

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdna?st=CS0CAP008AC05NP1&c=1683.f>.

## FEATURES

source

Location/Qualifiers

1..961

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0CAP008Y809"

/tissue\_type="THYMUS"

/clone\_lib="Homo sapiens THYMUS"

/notes="Vector: pCMVSPORT.6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

## ORIGIN

Query Match 15.7%; Score 110; DB 4; Length 961;

Best Local Similarity 83.6%; Pred. No. 1.5e-09;

Matches 122; Conservative 2; Mismatches 22; Indels 0; Gaps 0;

QY 16 TTTTCTTTTTCATGATTTTAAATAATATCAATTTCTTTTATTATTATTATTAATTT 75

Db 675 TTATTTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 734

QY 76 TTAAGTTTTCAGGTACATGTCGAAGTGCAGGTTAGTTACATATATACATGCGCCA 135

Db 735 TTAGTTTTCAGGTACATGTCGAAGTGCAGGTTAGTTACATATATACATGCGCCA 794

QY 136 TCGTGTGTGCTGCACCATTAATCT 161

Db 795 TCGTGTGTGCTGCACCATTAATCT 820

## RESULT 2

BZ598311/c

LOCUS

DEFINITION BZ598311 Human MCF7 breast cancer cell line library (MCF7\_1) Homo

sapiens genomic clone MCF7\_1-2368, genomic survey sequence.

ACCESSION BZ598311

VERSION BZ598311.1 GI:31506773

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 785)

AUTHORS Volik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q.,

Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P.,

Gray, J.W. and Collins, C.

End-sequence profiling: Sequence-based analysis of aberrant genomes

Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)

12788976

COMMENT Contact: Volik SV

Colin Collins' lab

UCSF Comprehensive Cancer Center

UCSF Box 0808, San Francisco, CA 94143-0808, USA

Tel: 415 502 7066

Fax: 415 502 5665

Email: svolik@cc.ucsf.edu

This clone is available from Amplicon Express

<http://www.genomex.com>

Class: BAC ends.

## FEATURES

source

Location/Qualifiers

1..785

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/clone="MCF7\_1-2368"

/sex="female"

/clone\_lib="Human MCF7 breast cancer cell line library

(MCF7\_1)"

/note="Vector: pECBAC1; Site 1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (<http://www.genomex.com>) using their standard procedure."

## ORIGIN

Query Match 15.3%; Score 107.4; DB 12; Length 785;

Best Local Similarity 73.0%; Pred. No. 4.4e-09;

Matches 138; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 16 TTTTCTTTTTCATGATTTTAAATAATATCAATTTCTTTTATTATTATTATTAATTT 75

Db 575 TTATTTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 516

QY 76 TTAAGTTTTCAGGTACATGTCGAAGTGCAGGTTAGTTACATATATACATGCGCCA 135

Db 515 TTAAGTTTTCAGGTACATGTCGAAGTGCAGGTTAGTTACATATATACATGCGCCA 456

QY 136 TCGTGTGTGCTGCACCATTAATCTCACATGAAGTTTAAAAATTTTAGTGACAGTTT 195

Db 455 TCGTGTGTGCTGCACCATTAATCTCACATGAAGTTTAAAAATTTTAGTGACAGTTT 396

QY 196 TAGTCATTT 204

Db 395 GTGTTTCT 387

## RESULT 3

BZ311

LOCUS

DEFINITION

BZ311

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Other\_GSSs: CIT-HSP-388D1.TF

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com) . BAC

end search page:

[http://www.tigr.org/tcdb/hungen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tcdb/hungen/bac_end_search/bac_end_search.html)

Seq primer: M13 Reverse

Class: BAC ends.

Location/Qualifiers

1..522

source



[illegible]

```

QY 68 TTATACCTTTAACTTTTAGGTCATGTCACAGTGTGCAGGTTAGTTCATATATATAC 127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 362 TTATAC-TTTAAGTTTTAGGTCATGTCACATTTGTGCAGGTTAGTTCATATATATAC 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 128 ATGTGCATGCTGCTGTGCTGACCCCAATTAACATCACAT 165
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 ATGTGCATGCTGCTGTGCTGACCCCAATTAACATCACAT 458
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
DB349127
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

DB349127 TRACH3 Homo sapiens cDNA clone TRACH3005808 3', mRNA
sequence.
DB349127
DB349127.1 GI:83258349
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 567)
Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamaashita,R., Yamamoto,J., Sekine,M., Teuritani,K., Wakaquri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanabe,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction;
Helix Research Institute (HRI); 5'-end one pass sequencing; HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing; RAB.

FEATURES
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="TRACH3005808"
            /tissue_type="trachea"
            /clone_lib="TRACH3"
            /note="Vector: pWE18SFL3"

ORIGIN
Query Match 14.7%; Score 102.6; DB 9; Length 567;
Best Local Similarity 91.5%; Pred. No. 3.2e-08;
Matches 108; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 44 TATCACTTTCTTTTATTTATTTATTTATTTATTTATTTAGTTTAGGTCATGTCGAAGTG 103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 125 TTTAAATTTTATTTATTTATTTATTTATTTATTTATTTAGTTTAGGTCATGTCACAACG 184
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 104 TGCAGGTTAGTTACATATATATACATGTCGCTGGTGTGTCACCCCAATTAACCTC 161
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 185 TGCAGGTTAGTTACATATATATACATGTCGCTGGTGTGTCACCCCAATTAACCTC 242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
AQL11354
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CIT-HSP-2382A15.TR CIT-HSP Homo sapiens genomic clone 2382A15,
genomic survey sequence.
AQL11354
AQL11354.1 GI:3488011
GSS.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 397)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Other GSSs: CIT-HSP-2382A15.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
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        1..397
            /organism="Homo sapiens"
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            /clone="2382A15"
            /sex="Male"
            /cell_type="Sperm"
            /clone_lib="CIT-HSP"
            /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
            HindIII"

ORIGIN
Query Match 14.6%; Score 102; DB 11; Length 397;
Best Local Similarity 77.8%; Pred. No. 4.1e-08;
Matches 123; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 4 TTTCACATAAAGTTTTTTTTTTTGTATGATTTTTTAATAAATATCATTTCTTTTATT 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 212 TTTCCTTTTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTATT 271
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 64 ATTATTATACCTTTTAAAGTTTATAGGTCATGTCGCAAGTGTGCAGGTTAGTTCATATAT 123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 272 TTTTATTATACCTTTTAAAGTTTATAGGTCATGTCGCAATTTGTGCAGGTTAGTTCATATGT 331
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 124 ATACATGTCCATGCTGGTGTGCTGCACCCCAATTAACCTC 161
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 332 ATACATGTCCATGCTGGTGTGCTGCACCCCAATTAACCTC 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
CX869873
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CX869873 HESCA_38_E04.g1_A037 NIH MGC_262 Homo sapiens cDNA clone
IMAGE:7474642 5', mRNA sequence.
CX869873
CX869873.1 GI:58553047
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

```

REFERENCE	Hominidae; Homo.
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-re@mail.nih.gov Tissue Procurement: BresaGen, Inc. CDNA Library Preparation: Express Genomics, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Laboratory for Genomics and Bioinformatics, University of Georgia Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM15783 row: i column: 08 Seq primer: JENREV (CAGGAACAGCTATGACC) High quality sequence stop: 506.
FEATURES	Location/Qualifiers
source	1..506
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	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clones="IMAGE:7474642"
	/sex="male"
	/tissue_types="embryonic stem"
	/cell_type="human embryonic stem cells"
	/cell_line="BG01"
	/lab_hosts="DH10B-T1 phage-resistant E. coli"
	/clone_lib="NIH MGC 262"
	/note="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV; RNA obtained from human embryonic stem cells isolated from the inner cell mass of blastocyst stage embryos and differentiated to an early neural progenitor cell type. Cell line id and NIH Registry designation is BG01. Positive for Nestin and Musashi expression. Passage number 18. cDNA primed using oligo-dT primer: 5'-pGACTAGTTTCGTAGCGAGCGGCC(C)(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. This primary library is non-normalized (normalized primary library is NIH MGC 259). It was constructed by Express Genomics (Frederick, MD). Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Note: this is a Mammalian Gene Collection library."
ORIGIN	
Query Match	14.6%; Score 102; DB 9; Length 506;
Best Local Similarity	85.6%; Pred. No. 4.le-08;
Matches 125; Conservative	0; Mismatches 20; Indels 1; Gaps 1;
QY	16 TTTT...TTTTCATGATTTTAATAAAATATCATTTCTTTTTATTATATATCTT 75
Db	16 TTTT...TTTTCATGATTTTAATAAAATATCATTTCTTTTTATTATATATCTT 75
QY	76 TTAAGTTT...TAGGGTACATGTGCAAGTGTCAGGTAGTTACATATATACATGTGCCA 135
Db	76 -TTAAGTTT...TAGGGTACATGTGCAAGTGTCAGGTAGTTACATATATACATGTGCCA 134
QY	136 TGCTGGTGTGCTGCACCCATTAACTC 161
Db	135 TGCTGGTGTGCTGCACCCATTAACTC 160
RESULT 9	
DA104597	
LOCUS	DA104597 BRACE3 Homo sapiens cDNA clone BRACE3018053 5', mRNA EST 02-NOV-2005
DEFINITION	sequence.
ACCESSION	DA104597
VERSION	DA104597.1 GI:78759434

KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 552)
AUTHORS	Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano.S. Identification of Transcriptional Modulation: Large-scale Diversification and Characterization of Putative Alternative Promoters of Human Genes
JOURNAL	Genome Res. 16 (1), 55-65 (2006)
PUBMED	16344560
COMMENT	Contact: Takao Isogai PLJ Project (HRI Team) Helix Research Institute 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: flj-cdna@nifty.com NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); CDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.
FEATURES	Location/Qualifiers
source	1..552
	/organism="Homo sapiens"
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	/db_xref="taxon:9606"
	/clone="BRACE3018053"
	/tissue_type="cerebellum"
	/clone_lib="BRACE3"
	/note="Vector: pME18SFL3"
ORIGIN	
Query Match	14.6%; Score 102; DB 9; Length 552;
Best Local Similarity	85.6%; Pred. No. 4e-08;
Matches 125; Conservative	0; Mismatches 20; Indels 1; Gaps 1;
QY	16 TTTT...TTTTCATGATTTTAATAAAATATCATTTCTTTTTATTATATATCTT 75
Db	334 TTATTTTATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTATTTATCTT 392
QY	76 TTAAGTTT...TAGGGTACATGTGCAAGTGTCAGGTAGTTACATATATACATGTGCCA 135
Db	393 TTAAGTTT...TAGGGTACATGTGCAAGTGTCAGGTAGTTACATATATACATGTGCCA 452
QY	136 TGCTGGTGTGCTGCACCCATTAACTC 161
Db	453 TGCTGGTGTGCTGCACCCATTAACTC 478
RESULT 10	
AQ884211	
LOCUS	AQ884211 421 bp DNA linear GSS 09-NOV-1999
DEFINITION	HS 5499 Bl G04 SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=9267 Col=7 Row=N, genomic survey sequence.
ACCESSION	AQ884211
VERSION	AQ884211.1 GI:6315678
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 421)

**AUTHORS** Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

**TITLE** Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

**PUBMED** 10449764

**COMMENT** Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm)) or from Resear h Genetics (info@resgen.com). BAC end Web Server: <http://www.htsc.washington.edu>  
Plate: 9267 row: N column: 7  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 421.

**FEATURES**

source  
1..421  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=9267 Col=7 Row=N"  
/sex="male"  
/clone\_lib="RPCI-11 Human Male BAC Library"  
/notes="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

**ORIGIN**

Query Match 14.5%; Score 101.8; DB 11; Length 421;  
Best Local Similarity 93.8%; Pred. No. 4.5e-08;  
Matches 106; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 49 TTTTCTTTTATTATTATATATATCTTTTAAAGTTTGGGTGACATGCGAAAGTGTGCG 108  
|||||  
Db 165 TTTTATTGTTATTATTATATATCTTTTAAAGTTTGGGTGACATGCGAAAGTGTGCG 224  
|||||

QY 109 GTTAGTTACATATATATACATGTGCCATGCTGGTGTGCTGCCCACTTAACCTC 161  
|||||  
Db 225 GTTAGTTACATATGATATACATGTGCCATGCTGGTGTGCTGCCCACTTAACCTC 277  
|||||

**RESULT 11**  
AG102621 681 bp DNA linear GSS 03-NOV-2001

**LOCUS** Pan troglodytes DNA, clone: PTB-105P19.F, genomic survey sequence.

**DEFINITION** AG102621

**ACCESSION** AG102621

**VERSION** AG102621.1 GI:167231138

**KEYWORDS** GSS.

**SOURCE** Pan troglodytes (chimpanzee)

**ORGANISM** Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Pan.

**REFERENCE** 1  
**AUTHORS** Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
BAC end sequences of Library PTB

**TITLE** Unpublished

**JOURNAL** 2 (bases 1 to 681)

**REFERENCE** Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
Direct Submission

**JOURNAL** Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpes@sc.riken.go.jp, URL:<http://hgp.gsc.riken.go.jp/>, Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

**COMMENT** PRIMERS  
Sequencing: -21M13

**LIBRARY**  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI

**FEATURES**

source  
1..681  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-105P19.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"

**ORIGIN**

Query Match 14.5%; Score 101.8; DB 14; Length 681;  
Best Local Similarity 81.4%; Pred. No. 4.3e-08;  
Matches 118; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 17 TTTTCTTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATATATCTTT 76  
|||||  
Db 120 TATTCTCTTTTATTATTTTAAATTTTAAATTTTAAATTTTATTATTATATCTTT 179  
|||||

QY 77 TAAATTTTAGGTACATGCGAAAGTGTGCAAGTGTAGTACATATATATACATGTGCCAT 136  
|||||  
Db 180 TAAATTTTAGGTACATGCGCAATTTGTCAGGTTAGTTACATATGATGATGATGTCAT 239  
|||||

QY 137 GCTGGTGTGCTGCCCACTTAACCTC 161  
|||||  
Db 240 GCTGGTGTGCTGCCCACTTAACCTC 264  
|||||

**RESULT 12**  
AQ527159 591 bp DNA linear GSS 18-MAY-1999

**LOCUS** CITBI-E1-260411.TF CITBI-E1 Homo sapiens genomic clone 260411, genomic survey sequence.

**DEFINITION** AQ527159

**ACCESSION** AQ527159

**VERSION** AQ527159.1 GI:4838919

**KEYWORDS** GSS.

**SOURCE** Homo sapiens (human)

**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

**REFERENCE** 1 (bases 1 to 591)

**AUTHORS** Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.

**TITLE** Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building

**JOURNAL** Unpublished (1997)

**COMMENT** Other GSSs: CITBI-E1-260411.TR  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbe@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC end search page: [http://www.tigr.org/tcdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html).  
Seq primer: M13-21





Db 318 AGGTTACATGCCACAATGTCAGGTTTGTACATATGTATACATGTGCCATGTTGGTGT 377  
Qy 145 GCTGCACCCATTAACT 160  
Db 378 GCTGCACCCATTAACT 393

RESULT 17  
AQ021610  
LOCUS  
DEFINITION AQ021610 417 bp DNA linear GSS 09-JUN-1998  
CIT-HSP-2311P19.TR CIT-HSP Homo sapiens genomic clone 2311P19,  
genomic survey sequence.  
ACCESSION AQ021610  
VERSION AQ021610  
KEYWORDS AQ021610.1 GI:3200346  
SOURCE GSS.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 417)  
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,  
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,  
Simon,M. and Venter,J.C.  
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map  
Building (1998)  
JOURNAL Unpublished (1998)  
COMMENT Other GSSs: CIT-HSP-2311P19.TF  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdadams@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
http://www.tigr.org/tldb/hungen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13 Reverse  
Class: BAC ends.  
Location/Qualifiers  
FEATURES  
source  
1..417  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clones="2311P19"  
/sex="Male"  
/cell\_type="Sperm"  
/clone\_lib="CIT-HSP"  
/note="Vector: pBelobAC11; Site\_1: HindIII; Site\_2:  
HindIII"

ORIGIN  
Query Match 14.4%; Score 100.6; DB 11; Length 417;  
Best Local Similarity 81.1%; Pred. No. 7.3e-08;  
Matches 129; Conservative 0; Mismatches 29; Indels 1; Gaps 1;  
Qy 2 TGTTTCACATAAAGTTTTTTTTTTTGATGATTTTATAATAATATCATCTTTCTTTTATA 61  
Db 103 TTTTTCCTATTTCATCTTCATTTTTTTTTTCTTTTATTTATTTATTTATTTATTTA 162  
Qy 62 TTATTATATATCTTTTAAGTTTATAGGGTACATGTGCAAGTGTGCAGGTAGTTACATAT 121  
Db 163 TTATTATATATAC-TTTAAGTTTATAGGGTACATGTGCAACATGTGCAGGTAGTTACATAT 221  
Qy 122 ATATACATGTGCCATGTGTTGCTGCTGCACCCATTAACT 160  
Db 222 GTATACATGTGCCATGTGTTGCTGCTGCACCCATTAACT 260

RESULT 18  
CB048927/c

LOCUS  
DEFINITION CB048927 225 bp mRNA linear EST 17-JAN-2003  
NISC\_g107f10.y1 NCI\_CGAP\_Pr28 Homo sapiens cDNA clone IMAGE:3271074  
5', mRNA sequence.  
ACCESSION CB048927  
VERSION CB048927.1 GI:27787214  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 225)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
cDNA Library Preparation:  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
info@image.llnl.gov  
Plate: L1AM8007 row: L column: 19  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
FEATURES  
source  
1..225  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3271074"  
/sex="male"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Pr28"  
/note="Organ: prostate; Vector: pT7T3D-PacI; Plasmid DNA  
from the normalized library NCI CGAP Pr22 was prepared,  
and ss circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(cloneIDs 985608-986759, 1101192-1101959, and  
1217928-1220615). Subtraction by Bento Soares and M.  
Fatima Bonaldo."

## ORIGIN

Query Match 14.3%; Score 100.4; DB 4; Length 225;  
Best Local Similarity 84.9%; Pred. No. 8.1e-08;  
Matches 124; Conservative 0; Mismatches 21; Indels 1; Gaps 1;  
Qy 16 TTTTCTTTTGTGATGATTTTATAATAATATCATCTTTCTTTTATATTATATATCTT 75  
Db 170 TTTTCTTTTGTGATGATTTTATAATAATATCATCTTTCTTTTATATTATATATCTT 112  
Qy 76 TTAAGTTTATAGGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATATATGCGCA 135  
Db 111 TTAAGTTTATAGGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATATGCGCA 52  
Qy 136 TGCTGGTGTGCTGCACCCATTAACTC 161  
Db 51 TGCTGGTGTGCTGCACCCATTAACTC 26

RESULT 19  
CB410332/c

LOCUS  
DEFINITION CB410332 233 bp mRNA linear EST 24-MAR-2003  
NISC\_nc11a06.y1 COGENE 6E MAX Homo sapiens cDNA clone IMAGE:5776426  
5', mRNA sequence.  
ACCESSION CB410332  
VERSION CB410332.1 GI:29167072  
KEYWORDS EST.





Fax: 301 838 0208  
 Email: mdadams@tigr.org  
 Clones are available from Research Genetics (info@resgen.com). BAC  
 end search page:  
[http://www.tigr.org/tldb/hungen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html).  
 Seq primer: M13 Reverse  
 Class: BAC ends.

## FEATURES

Location/Qualifiers  
 1..451  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clones="2373020"  
 /sex="Male"  
 /cell\_type="Sperm"  
 /clone\_lib="CIT-HSP"  
 /note="Vector: pBelobAC11; Site\_1: HindIII; Site\_2:  
 HindIII"

## ORIGIN

Query Match 14.3%; Score 100.4; DB 11; Length 451;  
 Best Local Similarity 84.9%; Pred. No. 7.8e-08;  
 Matches 124; Conservative 0; Mismatches 21; Indels 1; Gaps 1;  
 Oy 16 TTTTCTTTTGTGATGATTTTAAATAAATATACATTTCTTTTATTATTATTATATACCT 75  
 Db 122 TCTTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATAC-T 180  
 Oy 76 TTAAGTTTGTAGGTACATGTCGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 135  
 Db 181 TTAAGTTTGTAGGTACATGTCGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 240  
 Oy 136 TGCTGGTGTGCTGCACCCATTAACCTC 161  
 Db 241 TGCTGGTGTGCTGCACCCATTAACCTC 266

## RESULT 22

Al310239 541 bp mRNA linear EST 01-PEB-1999  
 LOCUS q075h12.x1 NCI\_CGAP\_Kids Homo sapiens cDNA clone IMAGE:1914407 3'  
 DEFINITION similar to contains LI.b1 LI repetitive element ;, mRNA sequence.  
 ACCESSION Al310239  
 VERSION Al310239.1 GI:4005110  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 1 (bases 1 to 541)  
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CCAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Insert Length: 614 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 456.

## JOURNAL

COMMENT

## REFERENCE

AUTHORS

TITLE

REMARK

COMMENT

/clone="IMAGE:1914407"  
 /tissue type="2 pooled tumors (clear cell type)"  
 /lab host="DH10B"  
 /clone\_lib="NCI\_CGAP\_Kids"  
 /note="Organ: kidney; Vector: pT73D-PacI; Site\_1: Not I;  
 Site\_2: Eco RI; 1st strand cDNA was primed with a Not I -  
 oligo (dT) primer [5',  
 AACTGGAAGAATTCGCGCGCAATATTTTTTTTTTTTTTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. Library  
 went through one round of normalization. Library  
 constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 14.3%; Score 100.4; DB 1; Length 541;  
 Best Local Similarity 84.9%; Pred. No. 7.8e-08;  
 Matches 124; Conservative 0; Mismatches 21; Indels 1; Gaps 1;  
 Oy 16 TTTTCTTTTGTGATGATTTTAAATAAATATACATTTCTTTTATTATTATTATACCT 75  
 Db 34 TTTTCTTTTGTGATGATTTTAAATAAATATACATTTCTTTTATTATTATTATAC-T 92  
 Oy 76 TTAAGTTTGTAGGTACATGTCGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCA 135  
 Db 93 TTAAGTTTGTAGGTACATGTCGCAAGTGTGCAGGTAGTTACATATATACATGTGCCA 152  
 Oy 136 TGCTGGTGTGCTGCACCCATTAACCTC 161  
 Db 153 TGCTGGTGTGCTGCACCCATTAACCTC 178

## RESULT 23

BC010517 1577 bp mRNA linear HTC 04-MAR-2003  
 LOCUS BC010517  
 DEFINITION Homo sapiens, clone IMAGE:4150580, mRNA.  
 ACCESSION BC010517  
 VERSION BC010517.1 GI:14714746  
 KEYWORDS HTC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 1 (bases 1 to 1577)  
 Strausberg, R.  
 Direct Submission  
 Submitted (10-JUL-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

## REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

NTI-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: David N. Louis, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amc@bcm.tmc.edu](mailto:amc@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,  
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAC Plate: 19 Row: a Column: 16  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Similarity but not  
 identity to protein  
 This clone has the following problem: retained intron.



Db  
276 TGTATACATGTGCCATGTGGTGTGCTGCACCCACTAATC 316

RESULT 27	AA344409/C	307 bp	mRNA	linear	EST 21-APR-1997
LOCUS	EST50301	Gall bladder	Homo sapiens	cDNA 5'	end similar to EST
DEFINITION	containing L1 repeat,	mRNA sequence.			
ACCESSION	AA344409				
VERSION	AA344409.1	GI:1996648			
KEYWORDS	EST.				

SOURCE OF SPECIES  
ORGANISM

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homidae; Homo.  
1 (bases 1 to 307)

REFERENCE  
AUTHORS

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,  
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D.,  
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Clai, C.,  
Clyne, P., A. Clifton, T.P., Corcoran, M.D., Ellis-Babcock, C., Espartero,  
J.

Raysonarai, R., Friedl, K., Cuccione, M.C., Zarewsky, P., Fine, L.D., Pittenger, D.L., Fittzugh, W.M., Fridman, J.L., Geoghegan, N.S., Glodde, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudke, D.W., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.P., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Mettsner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

**TITLE**  
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
**JOURNAL**  
Nature 377 (6547 Suppl.), 3-174 (1995)

FEATURES

Seq primer: M13 Reverse  
Location/Qualifiers

Email: arkerlavet@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Tel: 3018599056  
Fax: 3018599423

```
/sex="female"  
/dev_stage="adult, 25 yrs"  
/clone_lib="Gall bladder 1"  
/note="Organ: gall bladder; Vector: pBluescript SK-;  
Site 1: EcoRI. Site 2: XhoI"
```

Query Match	14.3%	Score 100;	DB 1;	Length 307;
Best Local Similarity	80.6%;	Pred. No. 9.4e-08;		
Matches 129;	Conservative 0;	Mismatches 30;	Indels 1;	Gaps 1;

  

QY	2	TGTTTCACATAAAGTTTTTTTTTTTGGATGATTTTAATAAAATATCATTTTCTTTTTTA	61
Db	240	TATTTTATTTATTTTATTTTGGTGGGTCCTTTCACTTTATGAAGTTTTTTTCTTTATTA	181
QV	62	TTATTTATTTACTTTTTTAAGTTTTTGGGTGATCATGTGCAAGTGTGCAGGTTAGTTACATAT	121

```

180 TTATTATTATAC-TTTAAGTTTGGGTACATGTGCACATATGCAGGTAGTTACATAT 122
|||||
122 ATATACATGCGCATGCTGGTGTGCGCACCCCAATTAATC 161
|||||
121 GTATACATGCGCATGCTAGTGTGCTGCACCCCAATTAATC 82
|||||

RESULT 28
CA947015/c
LOCUS
DEFINITION
CA947015
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 621)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,K., Cole,K., Tsagarisshvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: is10a12.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 481.
FEATURES
Source
1..621
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6364319"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/notes="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

Query Match 14.3%; Score 100; DB 4; Length 621;
Best Local Similarity 59.6%; Pred. No. 9.1e-08;
Matches 186; Conservative 0; Mismatches 125; Indels 1; Gaps 1;

49 TTTTCTTTTATTATATATATCTTTTAAAGTTTAGGTACATGCGCAAGTGTGCAG 108
|||||
435 TTTTATTATTTTATTTTATATATCTTTTAAAGTTTAGGTACATGCGCAAGTGTGCAG 376
|||||

```

```

QY 109 GTTAGTTACATATATACATGTCGATGCGTGGTGTGCGCACCCCAATTAACATGAA 168
|||||
Db 375 GTTGTGTTACATATATATACATGTCGATGCGTGGTGTGCGCACCCCAATTAACATGCT 316
|||||
QY 169 GTTTTTTTTAAATTTTAGTGACAGTTTTTAGTCTAATTTCTTAATTGAAAGTATCATAGTA 228
|||||
Db 315 CATTTTTTTT-TATTATACCTTTTATGCAAAATTAATTTAACTGCAATCCATCTTCTTGCTA 257
|||||
QY 229 ATCCATAAATTTGAAAAAATGTTAACTACTCTGTATATAAAAAAGTTTATAGTTTCTACT 288
|||||
Db 256 TCTTTCCCAATTCGCGTGTCTTCTCAAGTTTTTTTAAATTTTGTCTCTCCACTAATAGATA 197
|||||
QY 289 TTTAAGCAAAATTTCCATAGGCGATGTTAATGTTAGTTTCAACATTAATTTGCGAGTTTCAGT 348
|||||
Db 196 ATAATAAAGACCTCTTCTTTAAAGTTATTGGAAGTTTCAAAATACATCAATATTGAGA 137
|||||
QY 349 TAGTAAATAAAT 360
|||||
Db 136 CTAAACCAAAAT 125
|||||

RESULT 29
AQ052012
LOCUS
DEFINITION
AQ052012
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 672)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
Other GSSs: RPCI11-53B4.TK
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdamads@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
FEATURES
Source
1..672
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7519995"
/db_xref="taxon:9606"
/clone="RPCI-11-53B4"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/notes="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
RPCI11 Human Male BAC Library"

ORIGIN

Query Match 14.3%; Score 100; DB 11; Length 672;
Best Local Similarity 59.8%; Pred. No. 9e-08;
Matches 186; Conservative 0; Mismatches 125; Indels 1; Gaps 1;

```



Db 142 ATATTATAC-TTTAGTTTTAGGTACATGTGCACAGTGTGCAGGTAGTTACATATGT 200  
Qy 124 ATACATGTGCCATGCTGCTGTGCTGCACCACTTAATC 161  
Db 201 ATACATGTGCCATGCTGCTGTGCTGCACCACTTAATC 238

RESULT 32  
AG189910 352 bp DNA linear GSS 06-MAR-2004  
LOCUS Pan troglodytes DNA, clone: RP43-064003.T7, genomic survey  
DEFINITION  
ACCESSION AG189910 GI:45222086  
VERSION AG189910.1  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Pan.  
REFERENCE 1  
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J.,  
Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
BAC end sequences of Library RP-43  
Unpublished  
2 (bases 1 to 352)  
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J.,  
Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
Direct Submission  
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of  
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);  
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea  
(E-mail: redstone@mail.krribb.re.kr, URL: http://pns.grc.krribb.re.kr/,  
Tel: 82-42-866-7181, Fax: 82-42-860-4409)  
Clones are derived from the chimpanzee BAC library RP-43. This BAC  
end was generated during the R&D process and may have higher chance  
of clone tracking errors.  
PRIMERS  
Sequencing: T7  
LIBRARY  
Vector : pBACe3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI  
Location/Qualifiers  
1. 352  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="RP43-064003.T7"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone\_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN  
Query Match 14.2%; Score 99.4; DB 14; Length 352;  
Best Local Similarity 84.8%; Pred. No. 1.2e-07;  
Matches 123; Conservative 0; Mismatches 21; Indels 1; Gaps 1;  
Qy 18 TTTTCTTTTTCATGATTTTAAATAAATATCATTTCTTTTTTATTATTATTATTACTTTT 77  
Db 117 TTTTCTTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTAT 175  
Qy 78 AAGTTTTCAGGTACATGTCGCAATGTCAGGTAGTTAGTTACATATATATATGTCGCATG 137  
Db 176 AAGTTTTCAGGTACATGTCGCAATGTCAGGTAGTTAGTTACATATATATATGTCGCATG 235  
Qy 138 CTGGTGTGCTGCACCACTTAATCA 162  
Db 236 CTGGTGTGCTGCACCACTTAATCA 260

RESULT 33  
B92240 548 bp DNA linear GSS 09-APR-1999  
LOCUS RPC111-20K18.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-20K18,  
DEFINITION genomic survey sequence.  
ACCESSION B92240  
VERSION B92240.1 GI:2971351

DA502536 505 bp mRNA linear EST 04-NOV-2005  
LOCUS FCBBF3 Homo sapiens cDNA clone FCBBF3017123 5', mRNA  
DEFINITION  
ACCESSION DA502536  
VERSION DA502536.1 GI:80539325  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 505)  
Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,  
Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,  
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,  
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,  
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,  
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.  
Diversification of Transcriptional Modulation: Large-scale  
Identification and Characterization of Putative Alternative  
Promoters of Human Genes  
Genome Res. 16 (1), 55-65 (2006)  
16344560  
Contact: Takao Isogai  
FLJ Project (HRI Team)  
Helix Research Institute  
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: flj-cdna@ifty.com  
NEDO human cDNA project (New Energy and Industrial Technology  
Developmental Organization, Japan); cDNA library construction:  
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,  
Research Association for Biotechnology (RAB) and Biotechnology  
Center, National Institute of Technology and Evaluation; 3'-end one  
pass sequencing: RAB.  
FEATURES  
Location/Qualifiers  
1..505  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="FCBBF3017123"  
/tissue\_type="brain"  
/dev\_stage="fetal"  
/clone\_lib="FCBBF3"  
/note="Vector: pME18SFL3"

ORIGIN  
Query Match 14.2%; Score 99.4; DB 9; Length 505;  
Best Local Similarity 77.1%; Pred. No. 1.2e-07;  
Matches 121; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
Qy 6 TCACATAAAGTTTTTTTTTTTGATGATTTTAAATAAATATCATTTCTTTTTTTTAT 65  
Db 29 TCAATAAGCATTTGACCTTCCTTGGAACTTGCTCTCTTTCTTTTTTTTTTTTTT 88  
Qy 66 TATTATACCTTTTAAGTTTTAGGTACATGTGCAGGTGTCAGGTAGTTACATATATAT 125  
Db 89 AATTATACCTTTTAAGTCTTAGGTACATGTGCAGGTGTCAGGTGTTGTACGTATGAT 148  
Qy 126 ACATGTGCCATGCTGGTGTGCTGCACCACTTAATCA 162  
Db 149 ACATGTGCCATGCTGGTGTGCTGCACCACTTAATCA 185

RESULT 34  
B92240 548 bp DNA linear GSS 09-APR-1999  
LOCUS RPC111-20K18.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-20K18,  
DEFINITION genomic survey sequence.  
ACCESSION B92240  
VERSION B92240.1 GI:2971351



Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 906)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strauberg, Ph.D.  
Email: [rs9abs@mail.nih.gov](mailto:rs9abs@mail.nih.gov)

Tissue Procurement: Dr. James R. Lupski  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM13608 row: p column: 09  
High quality sequence stop: 554.

## FEATURES

Location/Qualifiers

1..906

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6198008"

/sex="male"

/tissue\_type="sciatic nerve"

/dev\_stage="adult, 70 yr"

/lab\_host="DH10B"

/clone\_lib="Lupski sciatic nerve"

/notes="Vector: pCMV-SPORT6 (Life Technologies); Site 1:  
NotI; Site 2: SalI; cDNA made by oligo-dT priming.  
Directionally cloned using the following adaptors:  
5'-TCGACCCACGCGTCCG-3' and  
5'-GACTAGTTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >  
1 kb for average insert length 1.87 kb. This is a primary  
library, non-amplified. Library constructed by Life  
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
College of Medicine) and is available through Life  
Technologies."

## ORIGIN

Query Match 14.2%; Score 99.4; DB 3; Length 906;  
Best Local Similarity 77.1%; Pred. No. 1.1e-07;  
Matches 121; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 6 TCACATTAAGCTTTTCTTTTTCATGATTTTAAATAAATCATCTTTCTTTTATATAT 65  
Db 207 TCAATAAGCATGACCTTCCTTGGAACTTCTTTCTTTTCTTTTCTTTTCTTTT 148

Qy 66 TATTATACCTTTTAACTTTTGGGTACATGTGCAAGTGCAGGTAGTTACATATATAT 125  
Db 147 AATTATACCTTTTAACTTTTGGGTACATGTGCAAGTGCAGGTAGTTACATATATAT 88

Qy 126 ACATGTGCCATGCTGTGTGCTGCACCCCAATTAACATCA 162  
Db 87 ACATGTGCCATGCTGTGTGCTGCACCCCAATTAACATCA 51

RESULT 37  
AQ319769  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AQ319769  
RPC11-10717-TV RPC1-11 Homo sapiens genomic clone RPC1-11-10717,  
genomic survey sequence.  
AQ319769  
AQ319769.1 GI:4052657  
GSS.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;  
Homiidae; Homo.

REFERENCE  
AUTHORS  
1 (bases 1 to 571)  
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,  
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

TITLE  
JOURNAL  
COMMENT

Use of human BAC End Sequences for Sequence-Ready Map Building  
Unpublished (1998)  
Other\_GSSs: RPC11-10717-TV  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: [hbe@tigr.org](mailto:hbe@tigr.org)

Clones are derived from the human BAC library RPC1-11. For BAC  
library availability, please contact Pieter de Jong  
([pieter@dejong.med.buffalo.edu](mailto:pieter@dejong.med.buffalo.edu)). Clones may be purchased from  
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from  
Research Genetics ([info@resgen.com](http://info@resgen.com)). BAC end search page:  
[http://www.tigr.org/tldb/hungen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html)  
Seq primer: T7  
Class: BAC ends.

## FEATURES

Location/Qualifiers

1..571

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="GDB:7540902"

/db\_xref="taxon:9606"

/clone="RPC1-11-10717"

/sex="Male"

/cell\_type="Lymphocytes"

/clone\_lib="RPC1-11"

/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;  
RPC111 Human Male BAC Library"

## ORIGIN

Query Match 14.2%; Score 99.2; DB 11; Length 571;  
Best Local Similarity 79.3%; Pred. No. 1.3e-07;  
Matches 130; Conservative 0; Mismatches 33; Indels 1; Gaps 1;  
Qy 20 TTTTTCATGATGATTTTAAATAAATCATCTTTCTTTTATTTATTTATTTATTTAA 79  
Db 246 TTGATATGTTTCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAC-TTTAA 304

Qy 80 GTTTTAGGTACATGTCACAAAGTGCAGGTAGTTACATATATATACATGTGCCATGCT 139  
Db 305 GTTTTAGGTACATGTCACAAAGTGCAGGTAGTTACATATATATACATGTGCCATGCT 364  
Qy 140 GGTGTCCTCACCCCAATCACTCATGAAGTTTCTTTTAAATTT 183  
Db 365 GGTGTCCTCACCCCAATCACTCATGAAGTTTCTTTTAAATTT 408

## RESULT 38

AQ446110

LOCUS

DEFINITION

AA446110 401 bp mRNA linear EST 03-JUN-1997  
zw60b03.s1 Soares total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone  
IMAGE:774413 3' similar to gb:L19872 AH RECEPTOR PRECURSOR  
(HUMAN); contains L1.b2 L1 repetitive element ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AA446110.1 GI:2158775  
EST.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;  
Homiidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 401)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Kucabota, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,  
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
White, Y., Wyllie, T., Waterston, R. and Wilson, R.  
WashU-Merck EST Project 1997  
Unpublished (1997)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108



Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -41m3 fwd. ET from AmerSham

High quality sequence stop: 369.

Location/Qualifiers

#### FEATURES

source

1..401

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:774413"

/dev\_stage="8-9 weeks"

/lab\_host="DH10B"

/clone\_lib="Soares total fetus Nb2HF9\_9w"

/note="Vector: pT73B-PacI; Site\_1: Not I; Site\_2: Eco RI;

1st strand cDNA was prepared from mRNA obtained from

pooled 8-9 week (total) fetus material with a Not I -

oligo(dT) primer [5,

TGTTACCAATCTGAAGTGGAGCGCCCTTAATTTTTTTTTTTT 3').

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo. "

#### ORIGIN

Query Match 14.1%; Score 99; DB 1; Length 401;

Best Local Similarity 86.5%; Pred. No. 1.4e-07;

Matches 122; Conservative 0; Mismatches 15; Indels 4; Gaps 1;

Qy 21 TTTTTCATCATGTTTATAAATATCATTTTCTTTTATTATTATTATTATTAAAG 80

Db 1 TTTTTCGAGATTTTATTATTATTATTATTATTATTATTATTATTATTATAC 56

Qy 81 TTTTAGGTACATGTCACAAAGTGCAGGTAGTTACATATATATACATGTCATGCTG 140

Db 57 TTTTAGGTACATGTCACAAAGTGCAGGTAGTTACATATATATACATGTCATGCTG 116

Qy 141 GTGTGTCACCCATTAACTC 161

Db 117 GTGTGTCACCCATTAACTC 137

#### RESULT 39

AQ029723

LOCUS

DEFINITION RPC111-41N20.TV RPC1-11 Homo sapiens genomic clone RPC1-11-41N20,

genomic survey sequence.

ACCESSION AQ029723

VERSION AQ029723.1 GI:3274854

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo

1 (bases 1 to 464)

REFERENCE Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,

Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and

Venter,J.C.

Use of BAC End Sequences for Sequence-Ready Map Building (1998)

Unpublished (1998)

CONTACT: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mhadams@tigr.org

Clones are derived from the human BAC library RPC1-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

source

1..464

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="GDB:7515691"

/db\_xref="taxon:9606"

/clone="RPC1-11-41N20"

/sex="Male"

/cell\_type="Lymphocytes"

/clone\_lib="RPC1-11"

/note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;

RPC111 Human Male BAC Library"

ORIGIN

Query Match 14.1%; Score 99; DB 11; Length 464;

Best Local Similarity 82.0%; Pred. No. 1.4e-07;

Matches 114; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 23 TTTTTCATGATTTTAAATAAATATCATTTTCTTTTATTATTATTATTATTAACTT 82

Db 81 TTTTTCGTGCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 140

Qy 83 TTAGGTACATGTCACAAAGTGCAGGTAGTTACATATATATACATGTCATGCTGCT 142

Db 141 TTAGGTACATGTCACATTTGTCAGGTAGTTACATATGATATATGTCATGCTGCT 200

Qy 143 GTGCTGCACCCATTAACTC 161

Db 201 GCGCTGCACCCACTAACTC 219

#### RESULT 40

DB302517/c

LOCUS

DEFINITION DB302517 BRAWY2 Homo sapiens cDNA clone BRAWY2030702 3', mRNA

sequence.

ACCESSION DB302517

VERSION DB302517.1 GI:83085415

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo

1 (bases 1 to 553)

REFERENCE Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,

Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,

Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,

Yoneyama,T., Osuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,

Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,

Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.

Diversification and Characterization of Putative Alternative

Splicing Sites in the Human Genome

Promoters of Human Genes

Genome Res. 16 (1), 55-65 (2006)

16344560

CONTACT: Takao Isogai

FLJ Project (HRI Team)

Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology

Developmental Organization, Japan); cDNA library construction:

Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,

Research Association for Biotechnology (RAB) and Biotechnology



```

Query Match      14.1%; Score 99; DB 11; Length 704;
Best Local Similarity 82.8%; Pred. No. 1.4e-07;
Matches 125; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

Qy 11 TAAAGTTTCTTTTTCATGATTTTATATAAATATCATTTCTCTTTTATATATATA 70
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
18 TATTTTATTTATTTATTTTCTCTATTAACATTTTATTTATTTATTTATTTATTA 77
Qy 71 TACTTTTAAAGTTTATAGGTACATGTGCAAGGTGCAGGTTAGTTACATATATACATG 130
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
78 TAC-GTTAAGTTTATAGGTACATGTGCACATGTGCAGGTTAGTTACATATATACATG 136
Qy 131 TGCCATGCTGTGTGCTGCACCCATTAAC TC 161
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
137 TTCCATGCTGTGTGCTGCACCCATTAAC TC 167

RESULT 43
Z36956
LOCUS
DEFINITION HBEA81M Atrium cDNA library Human heart Homo sapiens cDNA clone
HEA81M, mRNA sequence.
ACCESSION Z36956
VERSION Z36956.1 GI:535959
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 419)
AufRAY,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabakchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
757816
JOURNAL
PUBMED
COMMENT Contact: Genzentrum Muenchen
Laboratorium fuer molekulare Biologie
Am Klopferstritz 18a, 8033 Martinsried, Germany
Email: obermaier@vms.biochem.mpg.de
single read.

FEATURES
source
Location/Qualifiers
1..419
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEA81M"
/clone_lib="Atrium cDNA library Human heart"

ORIGIN
Query Match      14.1%; Score 98.8; DB 10; Length 419;
Best Local Similarity 89.8%; Pred. No. 1.5e-07;
Matches 106; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 44 TATCATTTCTTTTATTTATTTATTTATTTATTTTAAAGTTTATAGGTACATGCAAGTG 103
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
6 TATTTTATTTATTTTATTTTATTTATTTATTTATTTTAAAGTTTATAGGTACATGCAATG 65
Qy 104 TGCAGGTTAGTTACATATATACATGTGCCATGCTGTGTGCTGCACCCATTAAC TC 161
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
66 TGCAGGTTAGTTACATATATACATGTGCCATGCTGTGTGCTGCACCCATTAAC TC 123

RESULT 44
AQ042547/c
LOCUS
DEFINITION CIT-HSP-2328018.TR CIT-HSP Homo sapiens genomic clone 2328018,
genomic survey sequence.
ACCESSION AQ042547
VERSION AQ042547.1 GI:3309932

Query Match      14.1%; Score 99; DB 11; Length 704;
Best Local Similarity 82.8%; Pred. No. 1.4e-07;
Matches 125; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

Qy 11 TAAAGTTTCTTTTTCATGATTTTATATAAATATCATTTCTCTTTTATATATATA 70
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
18 TATTTTATTTATTTATTTTCTCTATTAACATTTTATTTATTTATTTATTTATTA 77
Qy 71 TACTTTTAAAGTTTATAGGTACATGTGCAAGGTGCAGGTTAGTTACATATATACATG 130
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
78 TAC-GTTAAGTTTATAGGTACATGTGCACATGTGCAGGTTAGTTACATATATACATG 136
Qy 131 TGCCATGCTGTGTGCTGCACCCATTAAC TC 161
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
137 TTCCATGCTGTGTGCTGCACCCATTAAC TC 167

RESULT 43
Z36956
LOCUS
DEFINITION HBEA81M Atrium cDNA library Human heart Homo sapiens cDNA clone
HEA81M, mRNA sequence.
ACCESSION Z36956
VERSION Z36956.1 GI:535959
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 419)
AufRAY,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabakchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
757816
JOURNAL
PUBMED
COMMENT Contact: Genzentrum Muenchen
Laboratorium fuer molekulare Biologie
Am Klopferstritz 18a, 8033 Martinsried, Germany
Email: obermaier@vms.biochem.mpg.de
single read.

FEATURES
source
Location/Qualifiers
1..419
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEA81M"
/clone_lib="Atrium cDNA library Human heart"

ORIGIN
Query Match      14.1%; Score 98.8; DB 10; Length 419;
Best Local Similarity 89.8%; Pred. No. 1.5e-07;
Matches 106; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 44 TATCATTTCTTTTATTTATTTATTTATTTATTTTAAAGTTTATAGGTACATGCAAGTG 103
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
6 TATTTTATTTATTTTATTTTATTTATTTATTTATTTTAAAGTTTATAGGTACATGCAATG 65
Qy 104 TGCAGGTTAGTTACATATATACATGTGCCATGCTGTGTGCTGCACCCATTAAC TC 161
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
66 TGCAGGTTAGTTACATATATACATGTGCCATGCTGTGTGCTGCACCCATTAAC TC 123

RESULT 44
AQ042547/c
LOCUS
DEFINITION CIT-HSP-2328018.TR CIT-HSP Homo sapiens genomic clone 2328018,
genomic survey sequence.
ACCESSION AQ042547
VERSION AQ042547.1 GI:3309932

```

```

KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 424)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
Unpublished (1998)
Other GSSs: CIT-HSP-2328018.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..424
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2328018"
/sex="Male"
/cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="vector: pBelOBAC11; Site_1: HindIII; Site_2:
HindIII"

ORIGIN
Query Match      14.1%; Score 98.8; DB 11; Length 424;
Best Local Similarity 79.6%; Pred. No. 1.5e-07;
Matches 129; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

Qy 1 CTGTTTCACATAAAGTTTCTTTTCTTTTATGATTTTAAATAAAATATCATTTCTTTT 60
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
298 CTGAGCCAAAGAGAAATAAAGCCCTTTTAAATTTATTTATTTATTTATTTATTTT 239
Qy 61 ATTATTATTATACTTTAAAGTTTATAGGTACATGTGCAAAAGTGTGCAGGTTAGTTACATA 120
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
238 ATTATTATTATAC-TTTAAGTTTATAGGTACATGTGCACAATGTGCAGGTTAGTTACATA 180
Qy 121 TATATACATGTGCCATGCTGTGTGCTGCACCCATTAAC TC 162
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
179 TGTATACATGTGCCATGCTGTGTGCTGCACCCATTAAC TC 138

RESULT 45
AQ127855
LOCUS
DEFINITION HS 3094 Al_B02_MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3094 Col=3 Row=C, genomic survey
sequence.
ACCESSION AQ127855
VERSION AQ127855.1 GI:3505021
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 468)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

```

Hood, L.  
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
10449764  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Sequence Tagged Connector  
Plate: 3094 row: C column: 3  
Class: BAC ends  
High quality sequence stop: 468.  
Location/Qualifiers  
1. .468  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="plate=3094 Col=3 Row=C"  
/sex="male"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"  
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

Query Match 14.1%; Score 98.8; DB 11; Length 468;  
Best Local Similarity 78.7%; Pred. No. 1.5e-07;  
Matches 118; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 11 TAAAGTTTTTTTTTTGATGATTTTAAATAAATATCATTTCTTTTATTATTATTA 70  
Db 95 TATTTTTTATTATTATTTTATTTTCAATATTTTATTATTATTATTGTTAAATT 154

QY 71 TACTTTTAGTTTTAGGTACATGTCGAAGTGTGCAGGTAGTACATATATACATG 130  
Db 155 ATACTTTAAGTTTTAGGTACATGTCGAATGTGCAGGTAGTACATATGACATG 214

QY 131 TGCCATGCTGGTGTGCTGCACCCATTAAC 160  
Db 215 TGACATGCTGGTGTGCTGCACCCACTAACT 244

RESULT 46  
AQ550918/c  
LOCUS  
DEFINITION  
RPCI-11-383F14.TV RPCI-11 Homo sapiens genomic clone  
RPCI-11-383F14, genomic survey sequence.  
ACCESSION  
AQ550918  
VERSION  
AQ550918.1 GI:4910095  
KEYWORDS  
GSS.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 561)  
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.  
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building  
Unpublished (1997)  
Other GSSs: RPCI-11-383F14.TJ  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbe@tigr.org  
Clones are derived from the human BAC library RPCI-11. For BAC

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
10449764  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Sequence Tagged Connector  
Plate: 3094 row: C column: 3  
Class: BAC ends  
High quality sequence stop: 468.  
Location/Qualifiers  
1. .468  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="plate=3094 Col=3 Row=C"  
/sex="male"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"  
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

Query Match 14.1%; Score 98.8; DB 11; Length 468;  
Best Local Similarity 78.7%; Pred. No. 1.5e-07;  
Matches 118; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 11 TAAAGTTTTTTTTTTGATGATTTTAAATAAATATCATTTCTTTTATTATTATTA 70  
Db 95 TATTTTTTATTATTATTTTATTTTCAATATTTTATTATTATTATTGTTAAATT 154

QY 71 TACTTTTAGTTTTAGGTACATGTCGAAGTGTGCAGGTAGTACATATATACATG 130  
Db 155 ATACTTTAAGTTTTAGGTACATGTCGAATGTGCAGGTAGTACATATGACATG 214

QY 131 TGCCATGCTGGTGTGCTGCACCCATTAAC 160  
Db 215 TGACATGCTGGTGTGCTGCACCCACTAACT 244

RESULT 46  
AQ550918/c  
LOCUS  
DEFINITION  
RPCI-11-383F14.TV RPCI-11 Homo sapiens genomic clone  
RPCI-11-383F14, genomic survey sequence.  
ACCESSION  
AQ550918  
VERSION  
AQ550918.1 GI:4910095  
KEYWORDS  
GSS.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 561)  
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.  
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building  
Unpublished (1997)  
Other GSSs: RPCI-11-383F14.TJ  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbe@tigr.org  
Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genet cs ([inforesgen.com](http://inforesgen.com)). BAC end search page: [http://www.tigr.org/tldb/hungen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html).  
Seq primer: T7  
Class: BAC ends.  
Location/Qualifiers  
1. .561  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/db\_xref="taxon:9606"  
/clone="RPCI-11-383F14"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/clone\_lib="RPCI-11"  
/note="Vector: pBACE3.6; Site\_1: EcoRI; Site\_2: EcoRI; RPCI11 Human Male BAC Library"

Query Match 14.1%; Score 98.8; DB 11; Length 561;  
Best Local Similarity 76.6%; Pred. No. 1.5e-07;  
Matches 121; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 4 TTTCATATAAGTTTTTTTTTTTGTGATGATTTTAAATAAATATCATTTCTTTTATT 63  
Db 479 TTAGCTGTCATGTTCTTTTCTTTTATTATTATTATTATTATTATTATTATT 420

QY 64 ATTATTATATCTTTTAAAGTTTTAGGGTACATGTGCAAAGTGTGCAGGTAGTTACATAT 123  
Db 419 TATTATTATATCTTTTAAAGTTTTAGGGTACATGTGCACAAATGTGCAGGTAGTTACATATGT 360

QY 124 ATACATGTCCCATGCTGTGCTGCACCCATTAAC 161  
Db 359 ATACATGTCCCATGCTGTGCTGCACCCATTAAC 322

RESULT 47  
BQ447264  
LOCUS  
DEFINITION  
UI-H-EU1-bad-1-23-0-UI.s1 NCI CGAP Ctl Homo sapiens cDNA clone  
UI-H-EU1-bad-1-23-0-UI 3', mRNA sequence.  
ACCESSION  
BQ447264  
VERSION  
BQ447264.1 GI:21250376  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 725)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Jose Mercuende  
cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu  
The following repetitive elements were found in this cDNA sequence: 1-48, >(TAAA)n#Simple repeat (matched complement) 51-169, >L1PA2#LINE/L1 (matched complement) 413-454, >AT rich#Low complexity 498-590, >MIR#SINE/MIR (matched complement)  
Seq primer: M13 FORWARD  
POLYA=yes.  
Location/Qualifiers  
1. .725  
/organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-EU1-bad-1-23-0-UI"
/tissue_type="Osteoarthritic Cartilage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ctl"
/note="Organ: Knee; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Ctl is a normalized cDNA library containing the
following tissue(s): Osteoarthritic Cartilage The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCAGCGT.
TAG_TISSUE=osteoarthritic cartilage
TAG_L1B=UI-H-EU1
TAG_SEQ=IGATCAGCGT"

```

# ORIGIN

```

Query Match      14.1%; Score 98.8; DB 3; Length 725;
Best Local Similarity 84.2%; Pred. No. 1.5e-07;
Matches 123; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

Qy 16 TTTTCTTTTTCGATGATTTAATAAAATATCATTTCTTTTATTATTATTACTT 75
    |||||
Db 2 TTTTCTTTTTCGATGATTTAATAAAATATCATTTCTTTTATTATTATTACTT 60
    |||||

Qy 76 TTAAGTTTTCAGGTACATGTCGAAGTGTGCAGGTAGTTACATATATATCATGTGCCA 135
    |||||
Db 61 TTAAGTTTTCAGGTACATGTCGAAGTGTGCAGGTAGTTACATATATATCATGTGCCA 120
    |||||

Qy 136 TGCTGGTGTGCTGCACCCCACTAACTC 161
    |||||
Db 121 TGCTGGTGTGCTGCACCCCACTAACTC 146
    |||||

```

```

RESULT 48
CZ446241/c
LOCUS      853 bp      DNA      linear      GSS      20-OCT-2005
DEFINITION MCF725h15TF Human MCF7 breast cancer cell line library (MCF7_1)
ACCESSION  C2446241
VERSION    C2446241.1 GI:77922503
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.

```

```

REFERENCE
AUTHORS    Volik,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brebner,J.H.,
            Bajsarowicz,K., Paris,P., Tao,Q., Kowbel,D., Lapuk,A.V., Kuo,W.-L.,
            Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de
            Jong,P., Pevzner,P. and Collins,C.
TITLE      Decoding the genomic architecture and high throughput detection of
            fusion transcripts in breast cancer cell lines: Implications for a
            tumor genome project

```

```

JOURNAL
COMMENT     Unpublished (2005)
            Contact: Volik SV
            Colin Collins' lab
            UCSF Comprehensive Cancer Center
            UCSF Box 0808, San Francisco, CA 94143-0808, USA
            Tel: 415 502 7066
            Fax: 415 502 5665
            Email: svolik@cc.ucsf.edu
            This clone is available from Amplicon Express

```

```

http://www.genomex.com
Class: BAC ends.
FEATURES             Location/Qualifiers
     source            1..853
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /clone="MCF7_25h15"
                        /sex="female"
                        /clone_lib="Human MCF7 breast cancer cell line library
                        (MCF7_1)"
                        /note="vector: pECBAC1; Site 1: HindIII; This library was
                        constructed from MCF7 breast cancer cell line by Amplicon
                        Express (http://www.genomex.com) using their standard
                        procedure."

```

# ORIGIN

```

Query Match      14.1%; Score 98.8; DB 13; Length 853;
Best Local Similarity 84.2%; Pred. No. 1.5e-07;
Matches 123; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

Qy 16 TTTTCTTTTTCGATGATTTAATAAAATATCATTTCTTTTATTATTATTACTT 75
    |||||
Db 228 TTTTCTTTTTCGATGATTTAATAAAATATCATTTCTTTTATTATTATTACTT 169
    |||||

Qy 76 TTAAGTTTTCAGGTACATGTCGAAGTGTGCAGGTAGTTACATATATATCATGTGCCA 135
    |||||
Db 168 -TAAAGTTTTCAGGTACATGTCGAAGTGTGCAGGTAGTTACATATATATCATGTGCCA 110
    |||||

Qy 136 TGCTGGTGTGCTGCACCCCACTAACTC 161
    |||||
Db 109 TGCTGGTGTGCTGCACCCCACTAACTC 84
    |||||

```

```

RESULT 49
BC032464/c
LOCUS      3088 bp      mRNA      linear      HTC      06-SEP-2002
DEFINITION Homo sapiens, clone IMAGE:5210997, mRNA.
ACCESSION  BC032464
VERSION    BC032464.1 GI:22749645
KEYWORDS   HTC.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.

```

```

REFERENCE
AUTHORS    Strausberg,R.
TITLE      Direct Submission
JOURNAL     Submitted (06-JUN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA

```

```

REMARK
COMMENT     NIH-MGC Project URL: http://mgc.nci.nih.gov
            Contact: MGC help desk
            Email: cgabs-x@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

```

Clone distribution: MSC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 64 Row: j Column: 2  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis  
This clone has the following problem: frame shifted.

## FEATURES

source  
1. .3088  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5210997"  
/tissue\_type="Blood, adult leukocytes"  
/clone\_lib="NIH\_MGC\_118"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"

## ORIGIN

Query Match 14.1%; Score 98.8; DB 6; Length 3088;  
Best Local Similarity 84.2%; Pred. No. 1.4e-07;  
Matches 123; Conservative 0; Mismatches 22; Indels 1; Gaps 1;  
  
QY 16 TTTTCTTTTTCATGATTTTAAATAAATATCATTTCTTTTTCATTTTATTTATTTATTTACTT 75  
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Db 3063 TTTTCTTTTTCATGATTTTAAATAAATATCATTTCTTTTTCATTTTATTTATTTATTTACTT 3005  
|||||  
  
QY 76 TTAAGTTTTCAGGTACATGTCGCAAGTGCACAGTTAGTTACATATATATACATGCGCCA 135  
|||||  
Db 3004 TTAAGTTTTCAGGTACATGTCGCAAGTGCACAGTTAGTTACATATATATACATGCGCCA 2945  
|||||  
  
QY 136 TGCTGGTGCTGCCACCATTAATCT 161  
|||||  
Db 2944 TGTGGTGCTGCCACCATTAATCT 2919  
|||||

## RESULT 50

AQ017761 324 bp DNA linear GSS 09-JUN-1998  
LOCUS  
DEFINITION  
CIT-HSP-2304A13.TR CIT-HSP Homo sapiens genomic clone 2304A13,  
genomic survey sequence.

## ACCESSION

VERSION  
AQ017761  
KEYWORDS  
GSS.

## SOURCE

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

## REFERENCE

AUTHORS  
1. (bases 1 to 324)  
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,  
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,  
Simon,M. and Venter,J.C.

## TITLE

Use of a random BAC End Sequence Database for Sequence-Ready Map  
Building (1998)

## JOURNAL

COMMENT  
Unpublished (1998)  
Other\_GSSs: CIT-HSP-2304A13.TF  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208

Email: [mdadams@tigr.org](mailto:mdadams@tigr.org)  
Clones are available from Research Genetics ([info@resgen.com](mailto:info@resgen.com)). BAC  
end search page:  
[http://www.tigr.org/tldb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html).  
Seq primer: M13 Reverse  
Class: BAC ends.

## FEATURES

source  
1. .324  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"

/db\_xref="taxon:9606"  
/clone="2304A13"  
/sex="Male"  
/cell\_type="Sperm"  
/clone\_lib="CIT-HSP"  
/note="Vector: pBelOBAC11; Site\_1: HindIII; Site\_2:  
HindIII"

## ORIGIN

Query Match 14.1%; Score 98.4; DB 11; Length 324;  
Best Local Similarity 79.1%; Pred. No. 1.8e-07;  
Matches 117; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
  
QY 12 AAAGTTTCTTTTTCATGATTTTAAATAAATATCATTTCTTTTTCATTTATTTATTTATTTAT 71  
|||||  
Db 142 AAAATTTTCTTTTTCATGATTTTAAATAAATATCATTTCTTTTTCATTTATTTATTTATTTAT 201  
|||||  
  
QY 72 ACTTTTAAGTTTTCAGGTACATGTCGCAAGTGCACAGTTAGTTACATATATATACATGTT 131  
|||||  
Db 202 TACTCTAAGTTTTCAGGTACATGTCGACATTTGGCAGGTTAGTTACATATGTTACATGTT 261  
|||||  
  
QY 132 GCATGCTGCTGCTGCTGCCACCATTAAC 159  
|||||  
Db 262 GCCATGCTGCTGCTGCTGCCACCATTAAC 289  
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## RESULT 51

AQ605001 398 bp DNA linear GSS 10-JUN-1999  
LOCUS  
DEFINITION  
HS 2119 B1 A12 T7C CIT Approved Human Genomic Sperm Library D Homo  
sapiens genomic clone Plate=2119 Col=23 Row=B, genomic survey  
sequence.

## ACCESSION

VERSION  
AQ605001.1  
KEYWORDS  
GSS.

## SOURCE

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

## REFERENCE

AUTHORS  
1. (bases 1 to 398)  
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
Hood,L.

## TITLE

Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

## JOURNAL

PUBMED  
10449764  
COMMENT  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887

Email: [jwallace@u.washington.edu](mailto:jwallace@u.washington.edu)  
Clones may be purchased from Research Genetics ([info@resgen.com](mailto:info@resgen.com)).  
BAC end Web Server: <http://www.htsc.washington.edu>  
Plate: 2119 row: B column: 23  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 398.

Location/Qualifiers  
1. .398  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=2119 Col=23 Row=B"  
/sex="male"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"  
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in  
E-Coli DH10B"

## FEATURES

source

1. .398  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=2119 Col=23 Row=B"  
/sex="male"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"  
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in  
E-Coli DH10B"

## ORIGIN



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ORIGIN
TAG_SEQ=GGCTGTAGGC"
Query Match      14.0%; Score 98.2; DB 3; Length 273;
Best Local Similarity 92.8%; Pred. No. 2e-07;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 TTTTCTTTTATTATTATATACATTTTAAAGTTTGGGTACATGTCGCAAGTGGCAG 108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 4 TTTTCTTTTATTATTATATACATTTTAAAGTTTGGGTACATGTCGCAAGTGGCAG 63

QY 109 GTTAGTTACATATATACATGTCGCAATGCTGTGCTGCACCCCACTAAC 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 64 GTTAGTTACATATGATACATGTCGCAATGCTGTGCTGCACCCCACTAAC 114

RESULT 54
AZ519511
LOCUS      555 bp      DNA      linear      GSS 16-OCT-2000
DEFINITION  RPCI-11-357P22.TJB RPCI-11 Homo sapiens genomic clone
ACCESSION  AZ519511
VERSION    AZ519511.1 GI:10831088
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 555)
AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
            BAC end sequences of library RPCI-11
            Unpublished (1997)
            Other GSSs: RPCI-11-357P22.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buhalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buhalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            This BAC end was generated during the R&D process and may have
            higher chance of clone tracking errors.
            Seq primer: SP6
            Class: BAC ends.
FEATURES
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            Location/Qualifiers
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                /mol_type="genomic DNA"
                /db_xref="GDB:7637085"
                /db_xref="taxon:9606"
                /clone="RPCI-11-357P22"
                /sex="Male"
                /cell_type="Lymphocytes"
                /clone_lib="RPCI-11"
                /notes="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
                RPC111 Human Male BAC Library"
ORIGIN
Query Match      14.0%; Score 98.2; DB 11; Length 555;
Best Local Similarity 78.1%; Pred. No. 1.9e-07;
Matches 118; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 11 TAAAGTTTCTTTTGGATGATTTTAAATAATATCATTTCTTTTATTATTATTA 70
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DB 51 TTATTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 110
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QY 71 TACTTTTAAAGTTTGGGTACATGTCGCAAGTGGCAGGTTAGTTACATATATACATG 130
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 111 ATACTTTTAAAGTTTGGGTGCAATGTCGCAATGTCGCAAGGTTAGTTACATATGATACATG 170
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 131 TGCCATGCTGGTGTGCTGCACCCCACTAAC 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 171 TGCCATGCTGGTGTGCTGCACCCCACTAAC 201
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 55
DB097926
LOCUS      560 bp      mRNA      linear      EST 10-DEC-2005
DEFINITION  DB097926 TEST14 Homo sapiens cDNA clone TEST14049307 5', mRNA
            sequence.
ACCESSION  DB097926
VERSION    DB097926.1 GI:83501773
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 560)
AUTHORS   Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
            Yoneyama,T., Otsuka,R., Kanda,T., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Morikawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
            Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
            Genome Res. 16 (1), 55-65 (2006)
            16344560
            Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES
    Location/Qualifiers
        1..560
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="TEST14049307"
            /tissue_type="testis"
            /clone_lib="TEST14"
            /note="Vector: pME18SFL3"
ORIGIN
Query Match      14.0%; Score 98.2; DB 9; Length 560;
Best Local Similarity 83.7%; Pred. No. 1.9e-07;
Matches 123; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

QY 16 TTTTCTTTTGGATGATTTTAAATAATATCATTTCTTTTATTATTATTATAC 75
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 378 TTCTATTGATTTGTTGTTGCTTATTTTCTTTTATTATTATTATTATAC-T 436
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 76 TTAAGTTTGGGTACATGTCGCAAGTGGCAGTTAGTTACATATATATACATGTCGCA 135
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 437 TTAAGTTTGGGTACATGTCGCAATGTCGCAATGTCGCAATGTCGCAATGTCGCA 496
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 136 TGTGTGTGCTGCACCCCACTAAC 162
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```



```

Db      497 TGCTGGTGTGCTGCCACCACTTAACCTCA 523

RESULT 56
BQ352132
LOCUS   IL3-HT0619-100700-208-A10 HT0619 Homo sapiens cDNA, mRNA sequence. EST 20-MAY-2002
DEFINITION
ACCESSION BQ352132
VERSION   BQ352132.1 GI:21016188
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE    Shotgun sequencing of the human transcriptome with ORF expressed
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED  10737800
COMMENT  Contact: Simpson A.J.G.
         Laboratory of Cancer Genetics
         Ludwig Institute for Cancer Research
         Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
         Brazil
         Tel: +55-11-2704922
         Fax: +55-11-2707001
         Email: asimpson@ludwig.org.br
         This sequence was derived from the FAPESP/LICR Human Cancer Genome
         Project. This entry can be seen in the following URL
         (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-HT0619-
         100700-208-A10&t3=2000-07-10&t4=1)
         Seq primer: puc 18 forward
         High quality sequence stop: 226.

FEATURES             Location/Qualifiers
     source            1..226
     -organism="Homo sapiens"
     -mol_type="mRNA"
     -db_xref="taxon:9606"
     -dev_stage="Adult"
     -clone_lib="HT0619"
     -note="Organ: head neck; Vector: puc18; Site 1: SmaI;
     Site 2: SmaI; A mini-library was made by cloning products
     derived from ORSTES PCR (U.S. Letters Patent application
     No. 196,716 - Ludwig Institute for Cancer Research)
     profiles into the pUC 18 vector. Reverse transcription of
     tissue mRNA and cDNA amplification were performed under
     low stringency conditions."

ORIGIN
Query Match      14.0%; Score 98; DB 3; Length 226;
Best Local Similarity 91.2%; Pred. No. 2.2e-07;
Matches 104; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy  49 TTTCTTTTATTATTATTATATCTTTTAAAGTTTAGGGGTACATGTGCAAGTGTGCAG 108
Db  107 TTAATTTTATTATTATTATTATATCTTTTAAAGTTTAGGGGTACATGTGCAAGTGTGCAG 166
Qy  109 GTTAGTTACATATATACATGTGCCATGCTGGTGTGCTGCCACCACTTAACCTCA 162
Db  167 GTTTGTTACATATGTATACATGTACCATGTTGGTGTGCTGCCACCACTTAACCTCA 220

RESULT 57
AQ628311
LOCUS   AQ628311
DEFINITION CITBI-E1-2650L21.TF CITBI-E1 Homo sapiens genomic clone 2650L21,

```

## Genomic survey sequence.

```

ACCESSION AQ628311
VERSION   AQ628311.1 GI:5090703
KEYWORDS GSS.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 480)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE    Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
JOURNAL Map Building
COMMENT  Other_GSSs: CITBI-E1-2650L21.TR
         Contact: Shaying Zhao, William Nierman, Mark Adams
         Department of Eukaryotic Genomics
         The Institute for Genomic Research
         9712 Medical Center Dr., Rockville, MD 20850
         Tel: 301 838 0200
         Fax: 301 838 0208
         Email: hbe@igr.org
         Clones are available from Research Genetics (info@resgen.com). BAC
         end search page:
         http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
         Seq primer: ML3-21
         Class: BAC ends.

FEATURES             Location/Qualifiers
     source            1..480
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     -mol_type="genomic DNA"
     -db_xref="taxon:9606"
     -clone="2650L21"
     -sex="male"
     -cell_type="sperm"
     -clone_lib="CITBI-E1"
     -note="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
     CalTech Human BAC Library D"

ORIGIN
Query Match      14.0%; Score 98; DB 11; Length 480;
Best Local Similarity 82.7%; Pred. No. 2.1e-07;
Matches 124; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

Qy  12 AAAGTTTTTTTTTTCATCATTTTATAAAATATCATTTTCTTTTTTATTATTATAT 71
Db  310 ATATTTTATCTATTGTTTGTGTAATTAATAATATTGTTTATTATTATTATTAT 369
Qy  72 ACTTTTAAAGTTTGGGTACATGTGCAAGTGTGCAGTTAGTTACATATATATACATGT 131
Db  370 ACTTTTAAAGTTTGGGTACATGTGCACATGTGCAGTTAGTTACATATGTATACCTGT 428
Qy  132 GCCATGCTGTGCTGCTGCCACCACTTAACCTC 161
Db  429 GCCATGCTGTGCTGCTGCCACCACTTAACCTC 458

RESULT 58
CR958489
LOCUS   CR958489
DEFINITION CR958489.1 GI:69955830
KEYWORDS GSS.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 740)

```

# AUTHORS

## TITLE

### JOURNAL

Schwarz, F., Neubert, P., Schneider, D., Peters, M. and Korn, B.  
 Direct Submission  
 Submitted (07-JUN-2005) RZPD Deutsches Ressourcenzentrum fuer  
 Genomforschung GmbH, Im Neuenheimer Feld 515, D-69120 Heidelberg,  
 Germany

#### COMMENT

RZPD: RZPDB737G0315D; RP3-416J7;  
 derived from Pieter J. de Jong library RPCI-3;  
 http://www.rzpd.de/cgi-bin/products/ci.cgi?CloneID=RZPDB737G0315D  
 RZPDB1B; (Human Genomic Set - RZPD 1.0) RZPD LIB No.737  
 http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=737  
 http://www.rzpd.de/products/genomicset/  
 Contact: Inge Airlart  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 100  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available from RZPD;  
 Contact RZPD (customer.service@rzpd.de) for further information.  
 Clone distribution: http://www.rzpd.de/products/genomicset/  
 Seq-primer: T7 (TAA-TAC-GAC-TCA-CTA-TAG-GG)  
 Class: BAC ends.

#### FEATURES

source  
 1. .740  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="RZPDB737G0315D"  
 /sex="Male"  
 /clone\_lib="RPCI-3"  
 /note="Vector: pCYPAC2; RPCI-3 Human Male PAC Library"

#### ORIGIN

Query Match 14.0%; Score 98; DB 14; Length 740;  
 Best Local Similarity 80.4%; Pred. No. 2e-07;  
 Matches 127; Conservative 0; Mismatches 30; Indels 1; Gaps 1;  
 QY 4 TTTACATATAAGTTTTTTTTTTTGTGATTTTAAATAAATATCATTTCTTTTATTT 63  
 Db 291 TTCATGTGAAGATTTGCTGCTTGTCTATTACATATTTATTGTTTCTTTTATTT 350  
 QY 64 ATTATTATACCTTTAAGTTTTAGGTACATGTGCAGAGTGCAGGTTAGTTACATATAT 123  
 Db 351 ATTATTATAC-TTTAAGTTTTAGGTACATGTGCAGATGTGCAGGTTAGTTACATATGT 409  
 QY 124 ATACATGTGCATGCTGGTGTGCTGCACCATTAACCTC 161  
 Db 410 ATACATGTGCATGCTGGTGTGCTGCACCTCATTAACCTC 447

#### RESULT 59

B75832 385 bp DNA linear GSS 08-APR-1999  
 LOCUS  
 DEFINITION  
 RPCI11-12116.TP RPCI-11 Homo sapiens genomic clone RPCI-11-12116,  
 genomic survey sequence.

#### ACCESSION

B75832

#### VERSION

B75832.1 GI:2771519

#### KEYWORDS

GSS.

#### SOURCE

Homo sapiens (human)

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

#### REFERENCE

1 (bases 1 to 385)

#### AUTHORS

Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,  
 Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and  
 Venter, J.C.

#### TITLE

Use of BAC End Sequences for Sequence-Ready Map Building

#### JOURNAL

Unpublished (1997)

#### COMMENT

Other\_GSSs: RPCI11-12116.TV  
 Contact: Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: mdaams@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  
 Research Genetics (info@resgen.com). BAC end search page:  
 http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html  
 Seq primer: SP6  
 Class: BAC ends.

#### FEATURES

Location/Qualifiers  
 source  
 1. .385  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="GDB:7504431"  
 /db\_xref="taxon:9606"  
 /clone="RPCI-11-12116"  
 /sex="Male"  
 /cell\_type="Lymphocytes"  
 /clone\_lib="RPCI-11"  
 /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;  
 RPCI11 Human Male BAC Library"

#### ORIGIN

Query Match 14.0%; Score 97.8; DB 11; Length 385;  
 Best Local Similarity 79.5%; Pred. No. 2.3e-07;  
 Matches 128; Conservative 0; Mismatches 32; Indels 1; Gaps 1;  
 QY 4 TTTACATATAAGTTTTTTTTTTTGTGATTTTAAATAAATATCATTTCTTTTATTT 63  
 Db 173 TTAGAAAGTGTTTTTTTTTTTTGTGTTTGAATTTGCGCATTTTATAATTTATTT 232  
 QY 64 ATTATTATACCTTTAAGTTTTAGGTACATGTGCAGAGTGCAGGTTAGTTACATATAT 123  
 Db 233 ACTATTATATAC-TTTAAGTTTTAGGTACGTGTGCACATGCGCAGGTTAGTTACATATGT 291  
 QY 124 ATACATGTGCCATGCTGGTGTGCTGCACCATTAACCTCACA 164  
 Db 292 ATACATGTCCGTGCTGGTGTGCTGCACCATTAACCTCAGA 332

#### RESULT 60

CR750736/c

#### LOCUS

DKFp470L1122.r1 470 (synonym: pliv1) Pongo pygmaeus cDNA clone  
 DKFp470L1122 5', mRNA sequence.

#### DEFINITION

CR750736

#### ACCESSION

CR750736

#### VERSION

CR750736.1 GI:51669903

#### KEYWORDS

EST.

#### SOURCE

Pongo pygmaeus (orangutan)

#### ORGANISM

Pongo pygmaeus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Pongo.

#### REFERENCE

1 (bases 1 to 657)

#### AUTHORS

Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,  
 Mewes, H.W., Weill, B., Amid, C., Osanger, A., Fobo, G., Han, M. and  
 Wiemann, S.

#### TITLE

Pongo pygmaeus mRNA (Poustka, A., Albert, R., Moosmayer, P., et al.)  
 Unpublished (2004)

#### JOURNAL

Contact: MIPS

#### COMMENT

MIPS  
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
 This is the 5' sequence of the clone insert from S. Wiemann,  
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);  
 Email s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD for  
 ordering:  
 http://www.rzpd.de/cgi-bin/products/ci.cgi?CloneID=DKFZp470L1122  
 Further information about the clone and the sequencing project is  
 available at http://mips.gsf.de/projects/cdna/.  
 Location/Qualifiers

[illegible]

	source	1..657 /organism="Pongo pygmaeus" /mol_type="mRNA" /db_xref="taxon:9600" /clone="DKFZp470L1122" /tissue_type="liver" /dev_stages="adult" /lab_host="DH10B" /clone_lib="470 (synonym: pliv1)" /note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
	ORIGIN	
	Query Match	14.0%; Score 97.8; DB 8; Length 657;
	Best Local Similarity	84.1%; Pred. No. 2.2e-07;
	Matches 122;	Conservative 0; Mismatches 22; Indels 1; Gaps 1;
QY	17	TTTTTTTTCATGATTTAATAAAATACATTTCTTTTTTATTATTATTATCATCTT 76
Db	159	TTTTTTTTTTTAGTGAGNAATTATCTTTTATTATTATTATTATTATTATAC-TT 101
QY	77	TAACTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCAT 136
Db	100	TAACTTTTAGGTACATGTGCACAATGTGCTGGTTAGTTACATATATATACATGTGCCAT 41
QY	137	GCTGTGTGCTGCACCATTAACTC 161
Db	40	GCTGTGTGCTGCACCATTAACTC 16
	RESULT 61	
	AFL18407	
	LOCUS	724 bp DNA linear GSS 21-FEB-2001
	DEFINITION	AFL18407 Homo sapiens skin ALU-PCR Homo sapiens genomic clone T2, genomic survey sequence.
	ACCESSION	AFL18407
	VERSION	AFL18407.1 GI:4325076
	KEYWORDS	GSS.
	SOURCE	Homo sapiens (human)
	ORGANISM	Homo sapiens
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo
	AUTHORS	Bertoni,F., Mullenbach,R., Broggini,M., Roggero,E., Cavalli,F., Cotter,F.E. and Zucca,E. Extranodal marginal zone B-cell lymphoma genotyping by Alu-polymerase chain reaction
	TITLE	Leuk. Lymphoma 38 (5-6), 605-610 (2000) 10953982
	JOURNAL	Contact: Bertoni F
	PUBMED	Dept. of Oncology
	COMMENT	Istituto di Ricerche Farmacologiche 'Mario Negri' via Eritrea 62, Milan, 20157, Italy absent in matched peripheral blood Class: Alu-PCR.
	FEATURES	Location/Qualifiers
	source	1..724 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="T2" /tissue type="skin" /cell type="primary marginal zone B-cell lymphoma" /clone lib="Homo sapiens skin ALU-PCR" /note="ALU-PCR fragment obtained with ALU4 primer"
	ORIGIN	
	Query Match	14.0%; Score 97.8; DB 11; Length 724;
	Best Local Similarity	77.5%; Pred. No. 2.2e-07;
	Matches 117;	Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY	12	AAAGTTTTTTTTTGTAGATTTTAATAAATATCATTTCTTTTTTATTATTATTAT 71
	Db	
	QY	76 TTAAGTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATACATGTGCCA 135
	Db	
	QY	16 TTTTTTTTTTTCATGATTTTAATAAAATATCATTTCTTTTTTATTATTATTACT 75
	Db	134 TTATTTATTTTTTTTATTATTATTTTTTTTATTATTATTATTATTATTACT 193
	QY	76 TTAAGTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATACATGTGCCA 135
	Db	
	QY	132 GCCATGCTGTGTGCGCACCCATTAACTCA 162
	Db	469 GCCATGTTGTGTGCGCACCCATCAACTCA 499
	RESULT 62	
	AQ464599	
	LOCUS	513 bp DNA linear GSS 23-APR-1999
	DEFINITION	HS_5104_B2_A11_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic_clone Plate=680 Col=22 Row=B, genomic survey sequence.
	ACCESSION	AQ464599
	VERSION	AQ464599.1 GI:4641694
	KEYWORDS	GSS.
	SOURCE	Homo sapiens (human)
	ORGANISM	Homo sapiens
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo
	AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
	TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
	JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
	PUBMED	10449764
	COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@jeng.med.buffalo.edu). Clones may be purchased from BACPAC Resources ( <a href="http://bacpac.med.buffalo.edu/ordering_bac.htm">http://bacpac.med.buffalo.edu/ordering_bac.htm</a> ) or from Resear h Genetics ( <a href="mailto:info@resgen.com">info@resgen.com</a> ). BAC end Web Server: <a href="http://www.htsc.washington.edu">http://www.htsc.washington.edu</a> Plate: 680 row: B column: 22 Seq primer: T7 Class: BAC ends High quality sequence stop: 513.
	FEATURES	Location/Qualifiers
	source	1..513 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="Plate=680 Col=22 Row=B" /sex="male" /clone lib="RPCI-11 Human Male BAC Library" /note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"
	ORIGIN	
	Query Match	13.9%; Score 97.6; DB 11; Length 513;
	Best Local Similarity	79.9%; Pred. No. 2.4e-07;
	Matches 115;	Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY	16	TTTTTTTTTTTCATGATTTTAATAAAATATCATTTCTTTTTTATTATTATTACT 75
Db	134	TTATTTATTTTTTTTATTATTATTTTTTTTATTATTATTATTATTATTACT 193
	QY	76 TTAAGTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATACATGTGCCA 135
	Db	
	QY	72 ACTTTTAAAGTTTTAGGGTACATGTGCAAAGTGTGCAGGTAGTTACATATATACATGT 131
	Db	409 TACITTTAAAGTTTTAGAGTACATGTGCAATGTGCGAGTTTGTGTACATATGTATACATGT 468
	Db	
	QY	349 AAAAGTTTTCCCACATATTATTATTATTATTTTACATAATAATTTTTTTTAAATNTATTATTATTA 408

	source	1..657 /organism="Pongo pygmaeus" /mol_type="mRNA" /db_xref="taxon:9600" /clone="DKFZp470L1122" /tissue_type="liver" /dev_stages="adult" /lab_host="DH10B" /clone_lib="470 (synonym: pliv1)" /note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
	ORIGIN	
	Query Match	14.0%; Score 97.8; DB 8; Length 657;
	Best Local Similarity	84.1%; Pred. No. 2.2e-07;
	Matches 122;	Conservative 0; Mismatches 22; Indels 1; Gaps 1;
QY	17	TTTTTTTTCATGATTTAATAAAATACATTTCTTTTTTATTATTATTATCATCTT 76
Db	159	TTTTTTTTTTTAGTGAGNAATTATCTTTTATTATTATTATTATTATTATAC-TT 101
QY	77	TAACTTTTAGGTACATGTGCAAGTGTGCAGGTAGTTACATATATATACATGTGCCAT 136
Db	100	TAACTTTTAGGTACATGTGCACAATGTGCTGGTTAGTTACATATATATACATGTGCCAT 41
QY	137	GCTGTGTGCTGCACCATTAACTC 161
Db	40	GCTGTGTGCTGCACCATTAACTC 16
	RESULT 61	
	AFL18407	
	LOCUS	724 bp DNA linear GSS 21-FEB-2001
	DEFINITION	AFL18407 Homo sapiens skin ALU-PCR Homo sapiens genomic clone T2, genomic survey sequence.
	ACCESSION	AFL18407
	VERSION	AFL18407.1 GI:4325076
	KEYWORDS	GSS.
	SOURCE	Homo sapiens (human)
	ORGANISM	Homo sapiens
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo
	AUTHORS	Bertoni,F., Mullenbach,R., Broggini,M., Roggero,E., Cavalli,F., Cotter,F.E. and Zucca,E. Extranodal marginal zone B-cell lymphoma genotyping by Alu-polymerase chain reaction
	TITLE	Leuk.Lymphoma 38 (5-6), 605-610 (2000)
	JOURNAL	10953982
	PUBMED	Contact: Bertoni F
	COMMENT	Dept. of Oncology Istituto di Ricerche Farmacologiche 'Mario Negri' via Eritrea 62, Milan, 20157, Italy absent in matched peripheral blood Class: Alu-PCR.
	FEATURES	Location/Qualifiers
	source	1..724 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="T2" /tissue type="skin" /cell type="primary marginal zone B-cell lymphoma" /clone_lib="Homo sapiens skin ALU-PCR" /note="ALU-PCR fragment obtained with ALU4 primer"
	ORIGIN	
	Query Match	14.0%; Score 97.8; DB 11; Length 724;
	Best Local Similarity	77.5%; Pred. No. 2.2e-07;
	Matches 117;	Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY	12	AAAGTTTTTTTTTGTGAATTTTAATAAATATCATTTCTTTTTTATTATTATTAT 71
	Db	
	QY	76 TTAAGTTTTAGGGTACATGTGCAAAGTGTGCAGGTAGTTACATATATACATGTGCCA 135
	Db	
	QY	72 ACTTTTAAAGTTTTTAGGGTACATGTGCAAAGTGTGCAGGTAGTTACATATATACATGT 131
	Db	
	QY	409 TACTTTAAAGTTTTTAGAGTACATGTGCAATGTGCAGTTTGTGTACATATGTATACATGT 468
	Db	
	QY	132 GCCATGCTGTGTGCTGCACCCATTAACTCA 162
	Db	
	QY	469 GCCATGTTGTGTGCTGCACCCATCAACTCA 499
	Db	
	RESULT 62	
	AQ464599	
	LOCUS	513 bp DNA linear GSS 23-APR-1999
	DEFINITION	HS_5104_B2_A11_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic_clone Plate=680 Col=22 Row=B, genomic survey sequence.
	ACCESSION	AQ464599
	VERSION	AQ464599.1 GI:4641694
	KEYWORDS	GSS.
	SOURCE	Homo sapiens (human)
	ORGANISM	Homo sapiens
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo
	AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
	TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
	JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
	PUBMED	10449764
	COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@jeng.med.buffalo.edu). Clones may be purchased from BACPAC Resources ( <a href="http://bacpac.med.buffalo.edu/ordering_bac.htm">http://bacpac.med.buffalo.edu/ordering_bac.htm</a> ) or from Resear h Genetics ( <a href="mailto:info@resgen.com">info@resgen.com</a> ). BAC end Web Server: <a href="http://www.htsc.washington.edu">http://www.htsc.washington.edu</a> Plate: 680 row: B column: 22 Seq primer: T7 Class: BAC ends High quality sequence stop: 513.
	FEATURES	Location/Qualifiers
	source	1..513 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="Plate=680 Col=22 Row=B" /sex="male" /clone lib="RPCI-11 Human Male BAC Library" /note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"
	ORIGIN	
	Query Match	13.9%; Score 97.6; DB 11; Length 513;
	Best Local Similarity	79.9%; Pred. No. 2.4e-07;
	Matches 115;	Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY	16	TTTTTTTTTTTGATGATTTTAAATAAAATATCATTTCTTTTTTATTATTATTA 75
Db	134	TTATTTATTTTTTTTATTATTTATTTTTTTTATTTTTGTGTTATTTTATTACT 193
	QY	76 TTAAGTTTTAGGGTACATGTGCAAAGTGTGCAGGTAGTTACATATATACATGTGCCA 135

Db 194 TTAAGTTTGGGTACATGTCACATGTCAGGTAGTACATATGATACATGTCCTCA 253  
 QY 136 TGCTGGTGTGCTGCACCACTTAAC 159  
 Db 254 TGCTGGTGTGCTGCACCACTTAAC 277

RESULT 63  
 C2465237 708 bp DNA linear GSS 20-OCT-2005  
 LOCUS MCF756k05TF Human MCF7 breast cancer cell line library (MCF7.1)  
 DEFINITION Homo sapiens genomic clone MCF7\_56k05, genomic survey sequence.

ACCESSION C2465237  
 VERSION C2465237.1 GI:77948426  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 708)  
 AUTHORS Volik,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brebner,J.H.,  
 Bajsarowicz,K., Paris,P., Tao,O., Kowbel,D., Lapuk,A.V., Kuo,W.-L.,  
 Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de  
 Jong,P., Pevzner,P. and Collins,C.

TITLE Decoding the genomic architecture and high throughput detection of  
 fusion transcripts in breast cancer cell lines: implications for a  
 tumor genome project  
 JOURNAL Unpublished (2005)  
 COMMENT Contact: Volik SV  
 Colin Collins' lab

UCSF Comprehensive Cancer Center  
 UCSF Box 0808, San Francisco, CA 94143-0808, USA  
 Tel: 415 502 7066  
 Fax: 415 502 5665  
 Email: avolik@cc.ucsf.edu  
 This clone is available from Amplicon Express  
 http://www.genomex.com  
 Class: BAC ends.

FEATURES  
 source Location/Qualifiers

1..708  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="MCF7\_56k05"  
 /sex="female"  
 /clone\_lib="Human MCF7 breast cancer cell line library  
 (MCF7.1)"  
 /note="Vector: pECBAC1; Site 1: HindIII; This library was  
 constructed from MCF7 breast cancer cell line by Amplicon  
 Express (http://www.genomex.com) using their standard  
 procedure."

ORIGIN  
 Query Match 13.9%; Score 97.6; DB 13; Length 708;  
 Best Local Similarity 77.6%; Pred. No. 2.4e-07;  
 Matches 118; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 10 ATAAAGTTTTTTTTTTGATGATTTTAAATAAATATCATTTCTTTTTTATTATTAT 69  
 Db 136 ATCACTTATTCATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 195

QY 70 ATACTTTTAAGTTTGGGTACATGTCGCAAGTGTGCAGGTAGTTACATATATACAT 129  
 Db 196 TATACTTTAAAGTTTGGGTACATGTCGCAAGTGTGCAGGTAGTTACATATACAT 255

QY 130 GTGCCATGCTGGTGTGCTGCACCACTTAAC 161

Db 256 GTGCCATGCTGGTGTGCTGCACCACTTAAC 287

RESULT 64

B72013  
 LOCUS B72013  
 DEFINITION B72013  
 ACCESSION B72013  
 VERSION B72013.1 GI:2711234  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 443)  
 AUTHORS Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,  
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and  
 Venter,J.C.

TITLE Use of BAC End Sequences for Sequence-Ready Map Building  
 JOURNAL Unpublished (1997)  
 COMMENT Other\_GSSs: RPC111-7E20.TP  
 Contact: Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208

Email: mdadams@tigr.org  
 Clones are derived from the human BAC library RPC1-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  
 Research Genetics (info@resgen.com). BAC end search page:  
 http://www.tigr.org/tdb/hungen/bac\_end\_search/bac\_end\_search.html  
 Seq primer: T7

Class: BAC ends.  
 Location/Qualifiers

1..443  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="GBB:7502419"  
 /db\_xref="taxon:9606"  
 /clone="RPC1-11-7E20"  
 /sex="Male"  
 /cell\_type="Lymphocytes"  
 /clone\_lib="RPC1-11"  
 /note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;  
 RPC111 Human Male BAC Library"

ORIGIN

Query Match 13.9%; Score 97.4; DB 11; Length 443;  
 Best Local Similarity 78.9%; Pred. No. 2.7e-07;  
 Matches 116; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 16 TTTTCTTTTCTTTGATGATTTTAAATAAATATCATTTCTTTTTTATTATTATTA 75  
 Db 260 TTTCTTTTCTTTCTTTTATTATTATTATTATTATTATTATTATTATTATTACT 319

QY 76 TTAAGTTTTAGGTACATGTCGCAAGTGTGCAGGTAGTTACATATATACATGTC 135  
 Db 320 TTAAGTTTTAGGTACATGTCGCAAGTGTGCAGGTAGTTACATATATACATG 379

QY 136 TGCTGGTGTGCTGCACCACTTAAC 162  
 Db 380 TGCTGGTGTGCTGCACCACTTAAC 406

RESULT 65

AG121371/c  
 LOCUS AG121371  
 DEFINITION Pan troglodytes DNA, clone: PTB-130G10.F, genomic survey sequence.  
 ACCESSION AG121371  
 VERSION AG121371.1 GI:16650536  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Pan.

REFERENCE 1  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Totoki, Y., Watanabe, H. and Sakaki, Y.  
BAC end sequences of Library PTB  
Unpublished

TITLE BAC end sequences of Library PTB

JOURNAL

REFERENCE 2  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Totoki, Y., Watanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: chimbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB. This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.

PRIMERS

Sequencing: -21M13

LIBRARY  
Vector : pKS145  
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R.Site 2 : SacI

FEATURES  
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Best Local Similarity 78.9%; Pred. No. 2.6e-07;  
Matches 116; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 16 TTTTCTTTTGTGATGATTTTAAATAAATATCATTTCTTTTATTATTATTATTAATT 75  
Db 431 TTATTAATTTTGTGCTCAAAACCAGTAATGCTTTCTTTTATTCTTTTATTCTTTTATTT 372

Qy 76 TTAAGTTTGTAGGTACATGTCACCAAGTGTGCAGTTAGTTACATATATATACATGTCGA 135  
Db 371 TTAAGTTTGTAGGTACATGTCACCAATGTGCAGTTTGTACATATGTATACATGTCGA 312

Qy 136 TGCTGGTGTGCTGCACCACTTAACCTCA 162  
Db 311 TGTTGGTGTACTGCACCACTTAACCTCA 285

RESULT 66  
CZ179389/7c 712 bp DNA linear GSS 31-JAN-2005

LOCUS AC105347Chiol\_tcl00.b1 Chimpanzee genomic DNA Pan troglodytes  
DEFINITION genomic, genomic survey sequence.

ACCESSION CZ179389  
VERSION CZ179389.1 GI:58347682

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Pan.

REFERENCE 1  
AUTHORS Hillier, L.W., Graves, T.A., Fulton, R.S., Fulton, L.A., Pepin, K.H.,  
Minx, P., Wagner-McPherson, C., Layman, D., Wyllie, K., Sekhon, M.,  
Becker, M.C., Fowell, G.A., Delehaanty, K.D., Miner, T.L., Nash, W.E.,  
Kremetzki, C., Oddy, L., Du, H., Sun, H., Bradshaw-Cordum, H., Ali, J.,

Carter, J., Cordes, M., Harris, A., Isak, A., van Brunt, A., Nguyen, C.,  
Du, F., Courtney, L., Kalicki, J., Ozersky, P., Abbott, S.,  
Armstrong, J., Belter, E.A., Caruso, L., Cedroni, M., Cotton, M.,  
Davidson, J., Desai, A., Elliott, G., Erb, T., Fronick, C., Gaige, T.,  
Haakenson, W., Haglund, K., Holmes, A., Harkins, R., Kim, K.,  
Kruchowski, S., Strong, C.M., Grewal, N., Goyea, E., Hou, S., Levy, A.,  
Martinka, S., Mead, K., McLellan, M.D., Meyer, R., Randall-Maher, J.,  
Tomlinson, C., Dauphin-Kohlberg, S. et al.  
Generation and annotation of the DNA sequences of human chromosomes  
2 and 4

TITLE Nature 434 (7034), 724-731 (2005)

JOURNAL 15815621

PUBMED

COMMENT Contact: Joanne Nelson  
Genome Sequencing Center  
Washington University School of Medicine  
4444 Forest Park Parkway, St. Louis, MO 63108, USA  
Tel: (314)286-1839  
Fax: (314)286-1810  
Email: submissions@watson.wustl.edu  
Class: PCR with specific primers.

FEATURES  
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Best Local Similarity 78.9%; Pred. No. 2.6e-07;  
Matches 116; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 15 GTTTTCTTTTTCATGATTTTAAATAAATATCATTTCTTTTATTATTATTATTAATTACT 74  
Db 693 GATTTTGTGAAGAAAGAAATTTAAAGGATTAATTCCTTTTCTTTTAAATATACC 634

Qy 75 TTTAAGTTTGTAGGTACATGTCACCAAGTGTGCAGTTAGTTACATATATATACATGTGCC 134  
Db 633 TTTAAGTTTGTGGGTACATGTCACATTTGTCAGTTTAGTTACATATGTATACATGTGCC 574

Qy 135 ATGCTGGTGTGTCGCCACCACTTAACCTC 161  
Db 573 ATGCTGGTGTGTCGCCACCACTTAACCTC 547

RESULT 67  
BZ610242 725 bp DNA linear GSS 08-JUN-2003

LOCUS WHADR41TF Human MCF7 breast cancer cell line library (MCF7.1) Homo  
DEFINITION sapiens genomic clone MCF7.1-23G10, genomic survey sequence.

ACCESSION BZ610242

VERSION BZ610242.1 GI:31518803

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Volik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q.,  
Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P.,  
Gray, J.W. and Collins, C.

TITLE End-sequence profiling: Sequence-based analysis of aberrant genomes

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)

PUBMED 12788976

COMMENT Contact: Volik SV  
Colin Collins' lab  
UCSF Comprehensive Cancer Center  
UCSF Box 0808, San Francisco, CA 94143-0808, USA  
Tel: 415 502 7066  
Fax: 415 502 5665  
Email: svolik@cc.ucsf.edu  
This clone is available from Amplicon Express

**ORIGIN**

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Query Match      13.9%; Score 97.4; DB 6; Length 995;
Best Local Similarity 87.4%; Pred. No. 2.5e-07;
Matches 118; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

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QY    490 TTATGATAAAAAATAATTTTTTTCTTTTTTTTATATATATATATADAC-TTTAAGTTTAG 548
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QY    87 GGTCATGTGCACAAGTGTCAGGTAGTTAGTTACATATATATACATGTGCCCATCGTGGTGTC 146
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QY    549 GGTACATGTGCACAATGTGCAGGTAGTTACATATGTATACATGTGCCATGCTGGTGGC 608
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QY    147 TGCACCCATTAATCT 161
Db     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY    609 TGCACCCACTAATCT 623
Db     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 69
BF954789/c
LOCUS          BF954789                238 bp mRNA linear EST 22-JAN-2001
DEFINITION    PM3-NN1203-151100-001-d08 NN1203 Homo sapiens cDNA, mRNA sequence.
ACCESSION     BF954789
VERSION       BF954789.1 GI:12372064
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE     1 (bases 1 to 238)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE         Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED       10737800
COMMENT       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM3&t2=PM3-NN1203-151100-001-d08&t3=2000-11-15&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 219.
Location/Qualifiers
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Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

FEATURES
source

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**ORIGIN**

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Query Match      13.9%; Score 97.2; DB 2; Length 238;

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